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OM protein - protein search, using sw model

Run on: August 19, 2004, 13:30:29 ; Search time 53 Seconds  
(without alignments)  
836.980 Million cell updates/sec

Title: US-09-716-356A-6  
Perfect score: 812  
Sequence: 1 YFGKLESKSLVRNLNDQVL.....LXKEDELGDRSMTFTVQNE 157

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A.Geneseq\_29Jan04.\*

1: geneseqp1980s.\*  
2: geneseqp1990s.\*  
3: geneseqp2000s.\*  
4: geneseqp2001s.\*  
5: geneseqp2002s.\*  
6: geneseqp2003as.\*  
7: geneseqp2003Bs.\*  
8: geneseqp2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	811	99.9	157	2 AAW77077	Human int
2	811	99.9	157	3 AAY57570	Human int
3	811	99.9	157	4 AAG65351	Human int
4	811	99.9	157	4 AAG65294	Human int
5	811	99.9	157	4 AAE06661	Human int
6	811	99.9	157	5 ABB04389	Human IL-
7	811	99.9	157	5 AAE17134	Human IL-
8	811	99.9	157	5 AAE16954	Human act
9	811	99.9	157	6 ABG73359	Human wil
10	811	99.9	157	6 ADA50616	Human mat
11	811	99.9	157	6 ADA50610	Human mat
12	811	99.9	157	6 ABR83372	Human int
13	811	99.9	157	7 ADE06775	Human int
14	811	99.9	158	3 AAY85167	Human int
15	811	99.9	177	6 ADA50614	Mature co
16	811	99.9	180	2 AAW48959	Wild-type
17	811	99.9	193	2 AAW22047	Interfero
18	811	99.9	193	2 AAW46592	Amino aci
19	811	99.9	193	4 AAB30541	A human I
20	811	99.9	193	4 AAG63830	Amino aci
21	811	99.9	193	5 AAE16953	Human pre
22	811	99.9	233	5 AAE16959	Ubiquitin
23	811	99.9	536	5 AAE16957	Human pro
24	811	99.9	588	5 AAE16958	Human pro
25	811	99.9	1048	5 AAE16960	Ubiquitin

## ALIGNMENTS

RESULT 1  
AAW77077  
ID AAW77077 standard; peptide; 157 AA.

XX AAW77077;  
XX AC  
XX DT 16-NOV-1998 (first entry)  
XX DE Human interleukin 18.  
XX DX  
XX KW Human; interleukin-18; IL-18; osteoclast; hypercalcaemia; osteopenia;  
KW KW osteoclastoma Behcet's syndrome; osteosarcoma; arthropathy; osteoporosis;  
KW KW chronic rheumatoid arthritis; deformity ostitis; primary hyperthyroidism.  
XX OS Homo sapiens.  
XX PN EP861663-A2.  
XX PD 02-SEP-1998.  
XX PF 24-FEB-1998; 98EP-00301352.  
XX PR 25-FEB-1997; 97JP-00055468.  
XX (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.  
XX PA Gillespie MT, Horwood NJ, Udagawa N, Kurimoto M;  
XX PI WPI; 1998-448964/39.  
XX DR N-PSDB; AAV48226.  
XX PT Use of interleukin-18 to inhibit osteoclast formation - in treatment of  
PT e.g. hypercalcaemia, osteoclastoma, Behcet's syndrome, osteosarcoma,  
PT chronic rheumatoid arthritis, deformity ostitis, primary hyperthyroidism  
XX and osteoporosis.  
XX PS Claim 4; Page 18; 56pp; English.  
XX CC Interleukin-18 (IL-18) or a functional equivalent can be used for  
CC inhibition of osteoclast formation. IL-18 is used for treating or  
CC preventing osteoclast-related diseases e.g. hypercalcaemia, osteoclastoma  
CC Behcet's syndrome, osteosarcoma, arthropathy, chronic rheumatoid  
CC arthritis, deformity ostitis, primary hyperthyroidism, osteopenia and  
XX osteoporosis  
XX SQ Sequence 157 AA;

Query Match 99.9%; Score 811; DB 2; Length 157;

Best Local Similarity 99.4%; Pred. No. 9.8e-83; Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		
QY	1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60	
Db	1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60	
QY	61 AVTISVKCEKISXLSCEKNKIIISFKEMNPPDNIKOTKSDIIFQRSVPGHDKMQPESY 120	
Db	61 AVTISVKCEKISXLSCEKNKIIISFKEMNPPDNIKOTKSDIIFQRSVPGHDKMQPESY 120	
QY	121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157	
Db	121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157	
RESULT 2		
AY57570	AY57570 standard; protein; 157 AA.	
ID	AY57570 standard; protein; 157 AA.	
XX	AC AAG65351;	
XX	AC AAG65351;	
DT	30-NOV-2001 (first entry)	
XX	DE Human interleukin-18 (IL-18) protein fragment.	
XX	DE Human interleukin-18 (IL-18) protein fragment.	
KW	IL-18; interleukin-18; human; antibody; antirheumatic; cerebroprotective;	
KW	nootropic; neurological; antiinflammatory; antiparkinsonian; cardiant;	
KW	immunosuppressive; antidepressant; neuroleptic; hepatotropic.	
OS	Homo sapiens.	
XX	WO200158956-A2.	
PN	16-AUG-2001.	
XX	09-FEB-2001; 2001WO-US004170.	
PF	10-FEB-2000; 2000US-0181608P.	
XX	(BADI ) BASF AG.	
XX	Chayur T, Dixon RW, Roguska M, White M, Labkovsky B, Salfeld J;	
PI	Duncan AR, Brocklehurst SM, Mankovich J, Shorrock CP, Thompson JE;	
PI	Lennard SN;	
XX	WPI; 2001-550020/61.	
DR	Novel antibodies and compounds capable of binding to human interleukin-18	
XX	useful for treating, e.g., inflammatory disorders, neurological	
PT	disorders, heart failure, myocardial infarction, and autoimmune diseases.	
PT	Dislosure; Page 14; 91pp; English.	
XX	The invention provides isolated antibodies, or antigen-binding portions,	
CC	that are capable of binding to human interleukin-18 (IL-18). The	
CC	antibodies may be used to inhibit human IL-18 activity in, and treat a	
CC	disorder where IL-18 is detrimental in, a human subject suffering from,	
CC	inflammatory disorders (e.g., rheumatoid arthritis, Crohn's disease,	
CC	inflammatory bowel disease, and osteoarthritis), neurological disorders	
CC	(e.g., Huntington's chorea, Parkinson's disease, Alzheimer's disease, and	
CC	stroke), heart failure, myocardial infarction, autoimmune diseases such	
CC	as autoimmune hepatitis and autoimmune neutropenia, and mental disorders	
CC	(e.g., depression and schizophrenia). Treatment with an anti-IL-18	
CC	antibody may occur before, concurrent, or after administration of a	
CC	second agent selected from an antibody, or fragment, capable of binding	
CC	human IL-12, methotrexate, anti-tumor necrosis factor, corticosteroids,	
CC	cyclosporin, rapamycin, FK506, and non-steroidal anti-inflammatory	
CC	agents. The present sequence represents a human IL-18 protein fragment	
XX	Sequence 157 AA;	
XX	Query Match 99.9%; Score 811; DB 4; Length 157;	
XX	Best Local Similarity 99.4%; Pred. No. 9.8e-83;	
XX	Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
QY	1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60	

Best Local Similarity 99.4%; Pred. No. 9.8e-83; Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		
QY	1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60	
Db	1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60	
QY	61 AVTISVKCEKISXLSCEKNKIIISFKEMNPPDNIKOTKSDIIFQRSVPGHDKMQPESY 120	
Db	61 AVTISVKCEKISXLSCEKNKIIISFKEMNPPDNIKOTKSDIIFQRSVPGHDKMQPESY 120	
QY	121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157	
Db	121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157	
RESULT 2		
AY57570	AY57570 standard; protein; 157 AA.	
ID	AY57570 standard; protein; 157 AA.	
XX	AC AAY57570;	
XX	AC AAY57570;	
DT	06-MAR-2000 (first entry)	
XX	DE Human interleukin 18 protein sequence SEQ ID NO:1.	
DE	Human; interleukin 18; IL-18; potentiator; IGIF; tumour; cancer;	
KW	interferon-gamma-inducing factor; growth inhibition; cytostatic.	
KW	Homo sapiens.	
OS	Homo sapiens.	
XX	WO9959565-A1.	
PN	25-NOV-1999.	
XX	20-MAY-1999; 99WO-US011160.	
PF	21-MAY-1998; 98US-0086560P.	
XX	(SMIK ) SMITHKLINE BEECHAM CORP.	
XX	Johnson RK;	
XX	WPI; 2000-062368/05.	
DR	New polypeptides, useful for preparation of composition for preventing	
XX	and/or treating cancer by inhibiting tumor growth.	
PT	Claim 1; Page 49-50; 53pp; English.	
PT	The present sequence represents human interleukin 18 (IL-18). The present	
XX	invention describes a compound comprising human or murine IL-18 in	
CC	combination with a chemotherapeutic agent (I). Also described are: (1) a	
CC	method of preventing and/or treating cancer in a mammal comprising the	
CC	administration of a cancer inhibiting amount of (I) comprising the IL-18	
CC	protein and the chemotherapeutic agent and optionally a pharmaceutically	
CC	acceptable carrier; and (2) a method of inhibiting the growth of tumour	
CC	cells in a mammal sensitive to a composition comprising human IL-18	
CC	and/or murine IL-18 and the chemotherapeutic agent (and optionally a	
CC	pharmaceutically acceptable carrier); comprising administering to a	
CC	mammal afflicted with the tumour cells an effective tumour cell growth	
CC	inhibiting amount of (I). The IL-18 protein in conjunction with a	
CC	chemotherapeutic agent is useful in a method for preventing and/or	
CC	treating cancer in mammals by inhibiting the growth of tumours or	
CC	cancerous cells in mammals	
XX	Sequence 157 AA;	
XX	Query Match 99.9%; Score 811; DB 3; Length 157;	
XX	Best Local Similarity 99.4%; Pred. No. 9.8e-83;	
XX	Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
QY	1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60	

Db 1 YFGKLESKLSVIRNLDQVLFIDQGNRPLFEDMTSDCRDNPRTIIFISMYKDSQPRGM 60  
QY 61 AVTISVKCEKISXLSKCNKIISFKEMNPPDNIKDTSKDIIFORSVPGHNDKNQFESSY 120  
Db 61 AVTISVKCEKISXLSKCNKIISFKEMNPPDNIKDTSKDIIFORSVPGHNDKNQFESSY 120  
QY 121 EGYFLACEKERDLFKLILKKEDELDGDRSIMFTVQNEED 157  
Db 121 EGYFLACEKERDLFKLILKKEDELDGDRSIMFTVQNEED 157

RESULT 4  
AAG65294  
ID AAG65294 standard; protein; 157 AA.  
XX AC AAG65294;  
XX DT 30-NOV-2001 (first entry)  
XX DE Human interleukin-18 (IL-18) protein fragment.  
XX KW IL-18; interleukin-18; human; antibody; antirheumatic; cerebroprotective;  
KW neurotropic; neurological; antiinflammatory; antiparkinsonian; cardiant;  
KW immunosuppressive; antidepressant; neuroleptic; hepatotropic.  
XX OS Homo sapiens.  
XX WO200158956-A2.  
XX PN 16-AUG-2001.  
XX PD 09-FEB-2001; 2001WO-US004170.  
XX PF 10-FEB-2000; 2000US-0181608P.  
XX PR (BADI ) BASF AG.  
XX PA Ghayur T, Dixon RW, Roguska M, White M, Labkovsky B, Salfeld J;  
PI Duncan AR, Brocklehurst SM, Mankovich J, Shorrock CP, Thompson JB;  
PI Lennard SN;  
XX WPI; 2001-550020/61.  
XX Novel antibodies and compounds capable of binding to human interleukin-18  
PT useful for treating, e.g., inflammatory disorders, neurological  
PT disorders, heart failure, myocardial infarction, and autoimmune diseases.  
XX Disclosure; Page 9; 91pp; English.  
XX The invention provides isolated antibodies, or antigen-binding portions,  
CC that are capable of binding to human interleukin-18 (IL-18). The  
CC antibodies may be used to inhibit human IL-18 activity in, and treat a  
CC disorder where IL-18 is detrimental in, a human subject suffering from,  
CC inflammatory disorders (e.g., rheumatoid arthritis, Crohn's disease,  
CC inflammatory bowel disease, and osteoarthritis), neurological disorders  
CC (e.g., Huntington's chorea, Parkinson's disease, Alzheimer's disease, and  
CC stroke), heart failure, myocardial infarction, autoimmune diseases such  
CC as autoimmune hepatitis and autoimmune neutropenia, and mental disorders  
CC (e.g., depression and schizophrenia). Treatment with an anti-IL-18  
CC antibody may occur before, concurrent, or after administration of a  
CC second agent selected from an antibody, or fragment, capable of binding  
CC human IL-12, methotrexate, anti-tumor necrosis factor, corticosteroids,  
CC cyclosporin, rapamycin, FK506, and non-steroidal anti-inflammatory  
CC agents. The present sequence represents a human IL-18 protein fragment  
XX  
SQ Sequence 157 AA;

Query Match 99.9%; Score 811; DB 4; Length 157;  
Best Local Similarity 99.4%; Pred. No. 9.8e-83;  
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLDQVLFIDQGNRPLFEDMTSDCRDNPRTIIFISMYKDSQPRGM 60

Db 1 YFGKLESKLSVIRNLDQVLFIDQGNRPLFEDMTSDCRDNPRTIIFISMYKDSQPRGM 60  
QY 61 AVTISVKCEKISXLSKCNKIISFKEMNPPDNIKDTSKDIIFORSVPGHNDKNQFESSY 120  
Db 61 AVTISVKCEKISXLSKCNKIISFKEMNPPDNIKDTSKDIIFORSVPGHNDKNQFESSY 120  
QY 121 EGYFLACEKERDLFKLILKKEDELDGDRSIMFTVQNEED 157  
Db 121 EGYFLACEKERDLFKLILKKEDELDGDRSIMFTVQNEED 157

RESULT 5  
AAE06661  
ID AAE06661 standard; protein; 157 AA.  
XX AC AAE06661;  
XX DT 16-OCT-2001 (first entry)  
XX DE Human interleukin-1gamma (IL-1gamma) protein.  
XX KW Human; interleukin-1gamma; IL-1gamma; virucide; hepatotropic; fever;  
KW immunological disorder; tumour; inflammatory disorder; hypoglycaemia;  
KW autoimmune disease; pulmonary tuberculosis; fulminant hepatitis; leprosy;  
KW psoriasis; viral infection; allergy; cytokine; HIV; drug screening.  
XX OS Homo sapiens.  
XX WO200157219-A2.  
XX PN 09-AUG-2001.  
XX PD 01-FEB-2001; 2001WO-US003285.  
XX PF 02-FEB-2000; 2000US-0179638P.  
XX PR (SCHE ) SCHERING CORP.  
XX PA Debets JEMA, Timans JC, Bazan JF, Kastelein RA;  
XX PI WPI; 2001-488886/53.  
XX DR Novel isolated or recombinant antigenic interleukin-1 delta or epsilon  
XX polypeptide useful for treating conditions exhibiting abnormal expression  
XX of interleukin such as immunological disorders, tumor and allergy.  
XX Disclosure; Fig 1; 103pp; English.  
XX The invention relates to recombinant antigenic interleukin-1 like  
CC molecules and their corresponding nucleic acid sequences, designated as  
CC interleukin-1delta (IL-1delta) and interleukin-1epsilon (IL-1epsilon). IL  
CC -1delta and IL-1epsilon are useful for treating conditions exhibiting  
CC abnormal expression of the interleukin such as immunological disorders,  
CC tumours, inflammatory disorders, fever, hypoglycaemia, psoriasis,  
CC allergy, autoimmune diseases and infectious diseases (e.g., pulmonary  
CC tuberculosis, leprosy, fulminant hepatitis, and viral infections such as  
CC HIV). The invention also relates to methods of using the composition  
CC containing IL-1delta or IL-1epsilon for both diagnostic and therapeutic  
CC utilities. IL-1delta is used as an immunogen for the production of  
CC antisera or antibodies specific, e.g., capable of distinguishing between  
CC IL-1 family members and an IL-1delta, for the interleukin or its  
CC fragment. The purified interleukin is used as a reagent to detect any  
CC antibodies generated in response to the presence of elevated levels of  
CC expression, or immunological disorders which lead to antibody production  
CC to the endogenous cytokine. The invention also contemplates the use of  
CC competitive drug screening assays. The present sequence is human  
CC interleukin-1gamma (IL-1gamma) protein related to the invention  
XX  
SQ Sequence 157 AA;

Query Match 99.9%; Score 811; DB 4; Length 157;  
Best Local Similarity 99.4%; Pred. No. 9.8e-83;

Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMVKDSQPRGM 60  
|||||  
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMVKDSQPRGM 60  
|||||

QY 61 AVTISVCKEIKSLSCENKIISFKEMNPPDNIKOTKSDIIFQSVPGHDNKMQFESSY 120  
|||||  
Db 61 AVTISVCKEIKSLSCENKIISFKEMNPPDNIKOTKSDIIFQSVPGHDNKMQFESSY 120  
|||||

QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157  
|||||  
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157  
|||||

## RESULT 6

ABB04389  
ID ABB04389 standard; protein; 157 AA.

AC ABB04389;

DT 21-MAY-2002 (first entry)

XX Human IL-18.

DE Human; IL-18; interleukin-18; cancer.

XX Homo sapiens.

XX CN1326992-A.

XX 19-DEC-2001.

XX 07-JUN-2000; 2000CN-00107993.

XX 07-JUN-2000; 2000CN-00107993.

XX (SHUA-) SHUANGU PHARM CO LTD BEIJING.

PI Xu M, Wang Y, Huang X;

XX WPI; 2002-217571/28.

DR N-PSDB; ABL41315.

XX Gene cloning, product preparation and use of Chinese interleukin-18  
PT subtype (53 Arg IL-18), useful for treating of cancer and other disease.

PS Claim 1; Page 7 (Disclosure); 8pp; Chinese.

XX The invention relates to the preparation of recombinant human interleukin  
CC -18 for treating of cancer and other disease

XX Sequence 157 AA;

Query Match 99.9%; Score 811; DB 5; Length 157;  
Best Local Similarity 99.4%; Pred. No. 9.8e-83;  
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMVKDSQPRGM 60  
|||||  
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMVKDSQPRGM 60  
|||||

QY 61 AVTISVCKEIKSLSCENKIISFKEMNPPDNIKOTKSDIIFQSVPGHDNKMQFESSY 120  
|||||  
Db 61 AVTISVCKEIKSLSCENKIISFKEMNPPDNIKOTKSDIIFQSVPGHDNKMQFESSY 120  
|||||

QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157  
|||||  
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157  
|||||

## RESULT 7

AAE17134.

ID AAE17134 standard; protein; 157 AA.

XX AAE17134;

AC AAE17134;

DT 22-APR-2002 (first entry)

XX Human IL-18 protein.

DE Human; viral disease; IL-18; interferon-gamma-inducing factor; IGIF; HSV;  
KW influenza virus; human immunodeficiency virus; HIV; herpes simplex virus;  
KW hepatitis A virus; HAV; hepatitis B virus; HBV; human papillomavirus;  
KW HPV; hepatitis C virus; HCV.

XX Homo sapiens.

OS WO200193898-AL.

XX 13-DEC-2001.

XX 01-JUN-2001; 2001WO-US017924.

XX 02-JUN-2000; 2000US-0208869P.

XX (SMIK ) SMITHKLINE BEECHAM CORP.

XX Esser KM, Rosenberg M, Tal-Singer R, Woodnutt G, Chisari FV;

XX WPI; 2002-154554/20.

XX Treatment of disease caused by e.g. influenza virus comprises  
PT administration of composition containing polypeptide, having identity of  
PT amino acid sequences.

XX Claim 1; Fig 1; 4lpp; English.

XX The invention relates to a method for treating viral diseases with IL-18,  
CC also known as interferon-gamma-inducing factor (IGIF) and IL-18  
CC combinations. The method involves administering a composition comprising  
CC IL-18 and IL-18 in combination with other agents. The method is used for  
CC treating diseases caused by viruses such as influenza virus, human  
CC immunodeficiency virus (HIV), herpes simplex virus (HSV), hepatitis A  
CC virus (HAV), hepatitis B virus (HBV), human papillomavirus (HPV) and  
CC hepatitis C virus (HCV). The present sequence is human IL-18 protein

SQ Sequence 157 AA;

Query Match 99.9%; Score 811; DB 5; Length 157;  
Best Local Similarity 99.4%; Pred. No. 9.8e-83;  
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMVKDSQPRGM 60  
|||||  
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMVKDSQPRGM 60  
|||||

QY 61 AVTISVCKEIKSLSCENKIISFKEMNPPDNIKOTKSDIIFQSVPGHDNKMQFESSY 120  
|||||  
Db 61 AVTISVCKEIKSLSCENKIISFKEMNPPDNIKOTKSDIIFQSVPGHDNKMQFESSY 120  
|||||

QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157  
|||||  
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157  
|||||

## RESULT 8

AAE16954  
ID AAE16954 standard; protein; 157 AA.

AC AAE16954;

DT 18-APR-2002 (first entry)

XX Human active interleukin-18 (IL-18) protein.

KW Human; interleukin-18; IL-18; caspase; interferon gamma; IFN-gamma;  
KW immunocompetent.  
XX Homo sapiens.  
XX WO200198455-A2.  
XX 27-DEC-2001.  
XX 11-JUN-2001; 2001WO-US018804.  
XX 15-JUN-2000; 2000US-0211832P.  
XX 10-AUG-2000; 2000US-0224128P.  
XX 20-JAN-2001; 2001US-0264923P.  
XX (SMIK ) SMITHKLINE BEECHAM CORP.  
XX Johanson KO, Kirkpatrick RB, Shatzman AR, Hoy YS, Mcdevitt P;  
XX WPI; 2002-139786/18.  
XX Activation of precursor polypeptide e.g. interleukin-18 polypeptide  
XX useful for inducing interferon-gamma production, comprises contacting or  
XX co-expressing caspase 4 or caspase 5 with precursor polypeptide.  
XX Claim 9; Fig 3; 64pp; English.  
XX The invention relates to a method for the in vitro activation of human  
XX precursor interleukin-18 (Pro-IL-18) with an activating enzyme. The  
XX method comprises contacting precursor IL-18 with an activating enzyme  
XX such as caspase 4 or caspase 5. Caspases 4 and 5 are members of a family  
XX of cysteine proteases that include interleukin-beta converting enzyme  
XX (ICE), which preferentially cleave substrates containing a protease  
XX activation motif. The methods are useful for producing physiologically  
XX active polypeptide e.g. active IL-18 polypeptide. The active IL-18  
XX polypeptide has an activity of inducing the production of interferon  
XX (IFN)-gamma in immunocompetent cells. IFN-gamma is useful as a  
XX biologically active substance for stimulating the production of IFNg from  
XX KG-1 (human myelomonocytic cell line) cells. The present sequence is  
XX human active IL-18 protein  
XX Sequence 157 AA;

Query Match 99.9%; Score 811; DB 5; Length 157;  
Best Local Similarity 99.4%; Pred. No. 9.8e-83;  
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLEDMTSDCDRNPRTFIISMVKDSQPRGM 60  
DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLEDMTSDCDRNPRTFIISMVKDSQPRGM 60  
QY 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIKDTSKDIIFQKSVPGHDKNMQFESSY 120  
DB 61 AVTISVKCEKISTLSCENKIISFKEMNPPDNIKDTSKDIIFQKSVPGHDKNMQFESSY 120  
QY 121 EGYFLACEKERDLFKLLKKEDELGRSINFTVQNE 157  
DB 121 EGYFLACEKERDLFKLLKKEDELGRSINFTVQNE 157

RESULT 9  
ABG73359  
ID ABG73359 standard; protein; 157 AA.  
XX AC ABG73359;  
XX DT 13-MAY-2003 (first entry)  
XX Human wild-type mature interleukin-18 (IL-18).  
XX Human; human interleukin-18; IL-18; IL-18 binding protein; IL-18BP;  
XX T helper type 1 response; Th1 response; cancer; viral disease;  
XX microbial infection; tumour immunotherapy; adjuvant; DNA vaccination;  
KW

KW graft versus tumour therapy; neutralisation; cytostatic; virucide;  
KW antimicrobial.  
XX Homo sapiens.  
XX US2002169291-A1.  
XX 14-NOV-2002.  
XX 08-MAR-2002; 2002US-00094153.  
XX 08-MAR-2001; 2001US-0274327P.  
XX (DINA/) DINARELLO C.  
XX (KIMS/) KIM S H.  
XX Dinarello C, Kim SH;  
XX WPI; 2003-298731/29.  
XX N-PSDB; ABX11788.  
XX Novel interleukin-18 mutant polypeptide useful in the treatment of cancer  
XX and viral disease, has mutations in amino acid residues which are  
XX involved in its interaction with IL-18 binding protein.  
XX Example 1; Fig 1B; 23pp; English.

XX The present invention relates to mutants of human interleukin-18 (IL-18)  
XX protein that have a lower affinity for IL-18 binding protein (IL-18BP)  
XX than the wild-type IL-18 protein. The IL-18 mutants of the invention  
XX comprise mutations in one or more amino acid residues which are involved  
XX in its interaction with IL-18BP. The mutations comprise substitutions,  
XX preferably non-conservative, additions or deletions. A pharmaceutical  
XX composition comprising an IL-18 mutant is useful for treating a disease  
XX which is prevented or alleviated by a T helper type 1 (Th1) response,  
XX including cancer and viral disease. The IL-18 mutants are useful in the  
XX treatment of the above diseases, microbial infections, in tumour  
XX immunotherapy, and as an adjuvant in DNA vaccination and in graft versus  
XX tumour therapy. The IL-18 mutants are resistant to, or less susceptible  
XX to, neutralisation than the wild-type protein. The present sequence  
XX represents human wild-type mature IL-18 protein  
XX Sequence 157 AA;

Query Match 99.9%; Score 811; DB 6; Length 157;  
Best Local Similarity 99.4%; Pred. No. 9.8e-83;  
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLEDMTSDCDRNPRTFIISMVKDSQPRGM 60  
DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLEDMTSDCDRNPRTFIISMVKDSQPRGM 60  
QY 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIKDTSKDIIFQKSVPGHDKNMQFESSY 120  
DB 61 AVTISVKCEKISTLSCENKIISFKEMNPPDNIKDTSKDIIFQKSVPGHDKNMQFESSY 120  
QY 121 EGYFLACEKERDLFKLLKKEDELGRSINFTVQNE 157  
DB 121 EGYFLACEKERDLFKLLKKEDELGRSINFTVQNE 157

RESULT 10  
ADA50616  
ID ADA50616 standard; protein; 157 AA.  
XX AC ADA50616;  
XX DT 20-NOV-2003 (first entry)  
XX Human mature consensus interleukin-18 (IL-18), SEQ ID NO:71.  
XX Nucleic acid vaccine; DNA vaccine; tumour antigen; cytokine adjuvant;  
XX humoral response; cellular response; immune response; immunotherapy;  
KW

Key	Location/Qualifiers
Misc-difference 4	/note= "Glu may replace wild-type Lys in a variant protein. A variant protein with this substitution would have changed activity compared to the wild-type protein"
Misc-difference 5	/note= "Val may replace wild-type Leu in a variant protein. A variant protein with this substitution is unlikely to have changed immunogenicity compared to the wild-type protein"
Misc-difference 6	/note= "Ile may replace wild-type Glu in a variant protein. A variant protein with this substitution would have changed activity compared to the wild-type protein"
Misc-difference 8	/note= "Asp may replace wild-type Lys in a variant protein. A variant protein with this substitution would have changed activity compared to the wild-type protein"
Misc-difference 10	/note= "Thr may replace wild-type Ser in a variant protein. A variant protein with this substitution would not have changed immunogenicity compared to the wild-type protein"
Misc-difference 12	/note= "Val may replace wild-type Ile in a variant protein. A variant protein with this substitution would not have changed immunogenicity compared to the wild-type protein"
Misc-difference 13	/note= "Ile may replace wild-type Arg in a variant protein. A variant protein with this substitution would have changed activity compared to the wild-type protein"
Misc-difference 15	/note= "Arg may replace wild-type Leu in a variant protein. A variant protein with this substitution would have changed activity compared to the wild-type protein"
Misc-difference 17	/note= "Lys may replace wild-type Asp in a variant protein. A variant protein with this substitution would have changed activity compared to the wild-type protein"
Misc-difference 20	/note= "Val or Ile may replace wild-type Leu in a variant protein. A variant protein with this substitution is unlikely to have changed immunogenicity compared to the wild-type protein"
Misc-difference 21	/note= "Tyr may replace wild-type Phe in a variant protein. A variant protein with this substitution is unlikely to have changed immunogenicity compared to the wild-type protein"
Misc-difference 22	/note= "Val may replace wild-type Ile in a variant protein. A variant protein with this substitution is unlikely to have changed immunogenicity compared to the wild-type protein"
Misc-difference 27	/note= "Lys may replace wild-type Arg in a variant protein. A variant protein with this substitution would have changed activity compared to the wild-type protein"
Misc-difference 30	/note= "Ala may replace wild-type Phe in a variant protein. A variant protein with this substitution would have changed activity compared to the wild-type protein"
Misc-difference 35	/note= "Lys may replace wild-type Asp in a variant protein. A variant protein with this substitution would have changed activity compared to the wild-type protein"
Misc-difference 37	/note= "Phe may replace wild-type Asp in a variant protein. A variant protein with this substitution would have changed activity compared to the wild-type protein"



KW mutant interleukin 18; MUT-IL-18; antiinflammatory; gene therapy;  
 XX inflammatory disorder.  
 XX Homo sapiens.  
 XX WO2003057821-A2.  
 XX 17-JUL-2003.  
 XX 25-OCT-2002; 2002WO-US034235.  
 XX 26-OCT-2001; 2001US-0335880P.  
 XX (CENZ ) CENTOCOR INC.  
 XX Heavner GA, Snyder LA, McCarthy SG;  
 XX WPI; 2003-577517/54.  
 XX New MUT-IL-18 nucleic acid, useful for preparing a composition for  
 PT diagnosing or treating a MUT-IL-18 related condition, e.g., inflammatory  
 PT disorder.  
 XX Example 3; Page 74; 97pp; English.  
 XX The present invention describes a mutant interleukin 18 (MUT-IL-18)  
 CC nucleic acid comprising or complementary to at least one polynucleotide  
 CC encoding an IL-18 amino acid sequence comprising at least one mutation  
 CC corresponding to at least one substitution selected from the group  
 CC consisting of Thr10 for Ser10, Val12 for Ile12, Ser45 for Thr45, Tyr47  
 CC for Phe47, Phe52 for Tyr52, Val64 for Ile64, Tyr101 for Phe101, Val15 for  
 CC Leu5, Val20 for Leu20, Ile20 for Leu20, Tyr21 for Phe21, Val22 for Ile22,  
 CC Ile66 for Val66, Thr72 for Ser72, or Phe148 for Ser148. Also described:  
 CC (1) a MUT-IL-18 polypeptide; (2) a MUT-IL-18 antibody; (3) a MUT-IL-18  
 CC vector comprising the MUT-IL-18 nucleic acid; (4) a MUT-IL-18 host cell  
 CC comprising the MUT-IL-18 nucleic acid; (5) a composition comprising a MUT  
 CC -IL-18 nucleic acid, polypeptide or antibody; (6) diagnosing or treating  
 CC a MUT-IL-18 related condition in a cell, tissue, organ or animal; (7) a  
 CC device comprising MUT-IL-18 nucleic acid, polypeptide or antibody and  
 CC that is suitable for contacting or administering the MUT-IL-18 nucleic  
 CC acid, polypeptide or antibody; (8) an article of manufacture for human  
 CC pharmaceutical or diagnostic use; and (9) producing the MUT-IL-18 nucleic  
 CC acid, polypeptide or antibody. MUT-IL-18 has antiinflammatory activity  
 CC and can be used in gene therapy. The MUT-IL-18 nucleic acid can be used  
 CC for preparing a composition for diagnosing or treating a MUT-IL-18  
 CC related condition, e.g. inflammatory disorder. The present sequence  
 CC represents a human IL-18 amino acid sequence given in an example from the  
 CC present invention  
 XX Sequence 157 AA;

Query Match 99.9%; Score 811; DB 6; Length 157;  
 Best Local Similarity 99.4%; Pred. No. 9.8e-83;  
 Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIIISMYKDSQPRGM 60  
 Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIIISMYKDSQPRGM 60  
 QY 61 AVTISVKCEKISXLSCKENKLIISFKEMNPPDNIKDTSKDIIFQORSVPCHDNKMQFESSY 120  
 Db 61 AVTISVKCEKISTLSCKENKLIISFKEMNPPDNIKDTSKDIIFQORSVPCHDNKMQFESSY 120  
 QY 121 EGYFLACEKERDLFKLILKKEDELGDRSINFVTQVNE 157  
 Db 121 EGYFLACEKERDLFKLILKKEDELGDRSINFVTQVNE 157

RESULT 13  
 ADE06775  
 ID ADE06775 standard; protein; 157 AA.  
 XX  
 AC ADE06775;

XX 29-JAN-2004 (first entry)  
 DT Human anti-diabetes Ig derived protein SEQ ID NO:3.  
 XX human; Ig; diabetes; complementarity-determining region; CDR;  
 DE antidiabetic; ophthalmological; neuroprotective; gene therapy;  
 XX diabetes mellitus; insulin resistance; hyperglycaemia; hypoglycaemia;  
 KW pancreatitis; Cushing's syndrome; acanthosis nigricans; retinopathy;  
 KW nephropathy; polyneuropathy; ulcer; infection.  
 XX Homo sapiens.  
 OS WO2003083071-A2.  
 XX 09-OCT-2003.  
 XX 26-MAR-2003; 2003WO-US009459.  
 XX 26-MAR-2002; 2002US-0367902P.  
 XX (CENZ ) CENTOCOR INC.  
 XX Griswold DE, Li J, Li L;  
 XX WPI; 2003-804047/75.  
 XX New isolated anti-diabetes immunoglobulin (Ig)-derived protein,  
 PT comprising at least one complementarity determining region (CDR) useful  
 PT for treating a diabetes-related condition, e.g. type I or II diabetes  
 PT mellitus, retinopathy.  
 XX Claim 1; SEQ ID NO 3; 84pp; English.  
 XX The invention relates to a novel isolated anti-diabetes immunoglobulin  
 CC (Ig)-derived protein, comprising at least one complementarity-determining  
 CC region (CDR). A protein of the invention has antidiabetic,  
 CC ophthalmological, and neuroprotective activity, and may have a use in  
 CC gene therapy. The protein, nucleic acid, composition and methods of the  
 CC invention are useful for treating a diabetes-related condition, e.g. type  
 CC I or II diabetes mellitus, insulin resistance, hyperglycaemia,  
 CC hypoglycaemia, pancreatitis, Cushing's syndrome, acanthosis nigricans,  
 CC retinopathy, nephropathy, polyneuropathy, ulcers, or infections. The  
 CC present sequence represents an anti-diabetes Ig derived protein of the  
 CC invention.  
 XX Sequence 157 AA;

Query Match 99.9%; Score 811; DB 7; Length 157;  
 Best Local Similarity 99.4%; Pred. No. 9.8e-83;  
 Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIIISMYKDSQPRGM 60  
 Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIIISMYKDSQPRGM 60  
 QY 61 AVTISVKCEKISXLSCKENKLIISFKEMNPPDNIKDTSKDIIFQORSVPCHDNKMQFESSY 120  
 Db 61 AVTISVKCEKISTLSCKENKLIISFKEMNPPDNIKDTSKDIIFQORSVPCHDNKMQFESSY 120  
 QY 121 EGYFLACEKERDLFKLILKKEDELGDRSINFVTQVNE 157  
 Db 121 EGYFLACEKERDLFKLILKKEDELGDRSINFVTQVNE 157

RESULT 14  
 AAY85167  
 ID AAY85167 standard; protein; 158 AA.  
 XX  
 AC AAY85167;  
 XX  
 DT 23-JUN-2000 (first entry)  
 XX



DE Human interleukin-18 (IL-18) amino acid sequence.  
XX  
KW Interleukin-18; production; IL-18; human; medical injection product.  
XX  
OS Homo sapiens.  
XX  
PN CN1243130-A.  
XX  
PD 02-FEB-2000.  
XX  
PF 24-JUL-1998; 98CN-00103307.  
XX  
PR 24-JUL-1998; 98CN-00103307.  
XX  
PA (WUGG/) WU G.  
XX  
PI Wu G, Liu Z;  
XX  
DR WPI; 2000-340020/30.  
XX  
DR N-PSDB; AAA10526.  
XX  
PT Preparation method for engineering bacteria for recombination of human  
XX leucocyte medium-18 and its product thereof.  
XX  
PS Claim 1; Page 2; 17pp; English.  
XX  
CC This sequence represents the human interleukin-18 (IL-18) amino acid  
CC sequence. The invention relates to a method for engineering bacterium for  
CC recombination of human IL-18 and a method for the preparation of IL-18. A  
CC primer containing a restriction endonuclease site can be used to  
CC accurately obtain the IL-18 gene containing 474 nucleotides, and uses the  
CC stop codon preferred by coli bacillus to raise the expression rate. The  
CC method uses a high-amplification culture medium to increase the  
CC expression level and only requires a one-step purification process to  
CC obtain a medical injection-pure product  
XX  
SQ Sequence 158 AA;  
Query Match 99.9%; Score 811; DB 3; Length 158;  
Best Local Similarity 99.4%; Pred. No. 9.9e-83;  
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTFIISMYKDSQPRGM 60  
Db 2 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTFIISMYKDSQPRGM 61  
QY 61 AVTISVKCEKISXLSCEKNIISFKENPPDNINKDTKSDIIFQFVSFGHDNKKMFESSY 120  
Db 62 AVTISVKCEKISTLSCENKIISFKENPPDNINKDTKSDIIFQFVSFGHDNKKMFESSY 121  
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157  
Db 122 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 158  
RESULT 15  
ADA50614  
ID ADA50614 standard; protein; 177 AA.  
XX  
AC ADA50614;  
XX  
DT 20-NOV-2003 (first entry)  
XX  
DE Mature consensus IL-18/LC signal sequence fusion protein, SEQ ID NO:69.  
XX  
KW Nucleic acid vaccine; DNA vaccine; tumour antigen; cytokine adjuvant;  
KW humoral response; cellular response; immune response; immunotherapy;  
KW cancer; cytostatic; vaccine; gene therapy; interleukin-18; IL-18; human.  
XX  
OS Chimeric.  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers

FT Peptide 1. -20  
FT /label= Human\_ILC\_signal\_sequence  
FT Protein 21..177  
FT /label= Mature\_consensus\_IL-18  
XX  
XX WO2003031569-A2.  
XX 17-APR-2003.  
XX  
XX 18-SEP-2002; 2002WO-US029640.  
XX  
XX 10-OCT-2001; 2001US-0328371P.  
XX  
XX (CENZ ) CENTOCOR INC.  
XX  
XX Snyder L, Scallan B, Knight DM, Mccarthy SG, Goletz TJ;  
XX Branigan PJ;  
XX  
XX WPI; 2003-393437/37.  
XX  
XX N-PSDB; ADA50611.  
XX  
XX New nucleic acid vaccine, useful for eliciting an immune response to a  
XX cancer associated tumor protein in a mammal.  
XX  
XX Claim 1b; Page 53; 92pp; English.  
XX  
XX The invention relates to a nucleic acid vaccine comprising one or more  
XX tumour antigen-encoding nucleic acids and one or more cytokine adjuvant-  
XX encoding nucleic acids. The tumour antigen encoded by the vaccine is  
XX mucin 1 (MUC-1), the kallikrein KLK2, or prostate specific antigen (PSA,  
XX also known as KLK3), and the cytokine adjuvant encoded can be interleukin  
XX -12 (IL-12), granulocyte macrophage-colony stimulating factor (GM-CSF),  
XX or especially interleukin-18 (IL-18). The antigen-encoding nucleic acid  
XX is preferably under the control of a promoter such as the cytomegalovirus  
XX immediate early promoter, the dihydrofolate reductase promoter or the  
XX early or late SV40 promoters. The invention also encompasses the method  
XX of eliciting an immune response to a tumour antigen in a mammal using the  
XX vaccine of the invention. Coexpression of the antigen and adjuvant  
XX induces a humoral or cellular response to the tumour antigen, generating  
XX an immune response useful for treatment or prophylaxis of cancers. The  
XX present sequence represents an interleukin-18 (IL-18) polypeptide which  
XX is specifically claimed for use in the vaccine of the invention.  
XX  
SQ Sequence 177 AA;  
Query Match 99.9%; Score 811; DB 6; Length 177;  
Best Local Similarity 99.4%; Pred. No. 1.2e-82;  
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTFIISMYKDSQPRGM 60  
Db 21 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTFIISMYKDSQPRGM 80  
QY 61 AVTISVKCEKISXLSCEKNIISFKENPPDNINKDTKSDIIFQFVSFGHDNKKMFESSY 120  
Db 81 AVTISVKCEKISTLSCENKIISFKENPPDNINKDTKSDIIFQFVSFGHDNKKMFESSY 140  
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157  
Db 141 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 177  
Search completed: August 19, 2004, 13:35:04  
Job time : 54 secs



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QM protein - protein search, using sw model

Run on: August 19, 2004, 13:33:10 ; Search time 16 Seconds  
(without alignments)  
943.879 Million cell updates/sec

Title: US-09-716-356A-6  
Perfect score: 812  
Sequence: 1 YFGKLESKLVIRNLNDQVL.....LKKEDELGRSIMFTVQNE 157

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues  
Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 78:\*  
1: Pir1:\*  
2: Pir2:\*  
3: Pir3:\*  
4: Pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	515	63.4	132	2 S60226	cytokine IGIF - mo
2	85	10.5	381	2 T40341	hypothetical prote
3	82	10.1	263	2 T39487	hypothetical prote
4	81.5	10.0	270	1 S10532	interleukin-1 alph
5	80.5	9.9	866	2 C71509	probable DNA polym
6	79	9.7	452	2 D64583	hypothetical prote
7	78.5	9.7	204	2 T44357	hypothetical prote
8	78	9.6	473	2 T32038	hypothetical prote
9	77.5	9.5	1251	2 A56677	neuroal cell cycl
10	77	9.5	364	2 A81261	probable periplasm
11	76	9.4	632	2 T00679	hypothetical prote
12	76	9.4	747	2 E84698	hypothetical prote
13	75.5	9.3	132	2 S15661	(2'-5')oligo(A) sy
14	75.5	9.3	270	2 T46620	interleukin-1 alph
15	75.5	9.3	1036	2 H64245	hypothetical prote
16	75.5	9.3	1663	1 C3MS	complement C3 prec
17	75	9.2	1064	1 S57450	protein-tyrosine k
18	75	9.2	2470	2 I50726	cation-independent
19	74.5	9.2	334	2 T04198	hypothetical prote
20	74.5	9.2	389	2 B69277	TRK potassum upta
21	74.5	9.2	467	2 A48713	serine/threonine-s
22	74.5	9.2	1228	2 A57384	multimerin, endoth
23	74.5	9.2	1510	2 T16927	hypothetical prote
24	74	9.1	245	2 B90488	hypothetical prote
25	74	9.1	361	2 E96904	mnd family Arpase
26	74	9.1	376	2 T24925	hypothetical prote
27	74	9.1	467	2 I49609	proto-oncogene pro
28	74	9.1	467	2 A47388	serine/threonine p
29	74	9.1	680	2 A28121	major merozoite su

30	74	9.1	810	2 B71639	virb4 protein prec
31	74	9.1	1772	2 A45532	major merozoite su
32	73.5	9.1	268	2 H85641	probable small sub
33	73.5	9.1	268	2 C90781	probable small sub
34	73	9.0	418	2 D82932	seryl-tRNA synthet
35	73	9.0	447	2 T26293	hypothetical prote
36	72.5	8.9	268	1 B24073	interleukin-1 alph
37	72.5	8.9	313	2 C96528	protein F27J15.10
38	72.5	8.9	436	2 G97701	polynucleotide ade
39	72.5	8.9	475	2 T32036	hypothetical prote
40	72.5	8.9	888	2 A38539	pl01 protein precu
41	72.5	8.9	1246	2 S60954	probable membrane
42	72.5	8.9	1294	2 T48349	KIN2 protein - Ara
43	72.5	8.9	1997	2 F71607	DNA helicase II BR
44	72	8.9	284	2 B90051	hypothetical prote
45	72	8.9	1613	2 S39059	protein BRG1 - hum

ALIGNMENTS

RESULT 1 0

S60226

Cytokine IGIF - mouse

C;Species: Mus musculus (house mouse)

C;Date: 10-Apr-1996 #sequence\_revision 19-Apr-1996 #text\_change 20-Jun-2000

C;Accession: S60226

R;Okamura, H.; Tsutsui, H.; Komatsu, T.; Yutsudo, M.; Hakura, A.; Tanimoto, T.; Torigoe,

Nature 378, 88-91, 1995

A;Title: Cloning of a new cytokine that induces IFN-gamma production by T cells.

A;Reference number: S60226; MUID:96061009; PMID:7477296

A;Accession: S60226

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-192 <OKA>

A;Cross-references: EMBL:D49949; NID:g1064822; PIDN:BAA08705.1; PID:g1064823

C;Superfamily: Mus musculus cytokine IGIF

Query Match 63.4%; Score 515; DB 2; Length 192;

Best Local Similarity 64.9%; Pred. No. 2.8e-42;

Matches 100; Conservative 27; Mismatches 25; Indels 2; Gaps 2;

QY 2 FGLKLESLVIRNLNDQVLFDQGNPLPDMEDMTDSCRNAPRTIIFIISMYKDSQRGMA 61

Db 37 FGLRHCTTAVIRINDQVLFDVK-RQVPFDMTDIDQSAEPQTRLIIYMKDSEVRGLA 95

QY 62 VTISVCKEIKSLSCENKIISFKEMNPPDNIDKTDIIFQSFVPHDNKMFESSSYE 121

Db 96 VTLSVDSKMSLTSLCKNKIISFEEMDPENIDDIQSDLIFFQKRVPGH-NKMFESSLYE 154

QY 122 GYFLACEKERDLFKLILKKEDLGDRSIMFTVQN 155

Db 155 GHFLACQKEDDAFKLILKKDKENGKSVNFTLTN 188

RESULT 2

T40341

hypothetical protein SPBC3B9.02c - fission yeast (Schizosaccharomyces pombe)

C;Species: Schizosaccharomyces pombe

C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 03-Dec-1999

C;Accession: T40341

R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Skelton, J.; Churcher, C.M.

submitted to the EMBL Data Library, March 1997

A;Reference number: Z21922

A;Accession: T40341

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-381 <WOO>

A;Cross-references: EMBL:AL022070; PIDN:CAAL7782.1; GSPDB:GN00067; SPDB:SPBC3B9.02c

A;Experimental source: strain 972h-; cosmid c3B9

C;Genetics:

A;Gene: SPDB:SPBC3B9.02c

A;Map position: 2

Query Match 10.5%; Score 85; DB 2; Length 381;  
Best Local Similarity 26.4%; Pred. No. 1.6;  
Matches 39; Conservative 23; Mismatches 54; Indels 32; Gaps 7;  
QY 3 GKLESKLVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIIISMVKDSQPRGMV 62  
DB 208 QQLSKDAF--DVNRPTFLGKAPVSELTDELINPKKTP----- 250  
QY 63 TISVK-CRKISXLSKSCNIIISF-KEMNPPDNIKDTKSDIIFQRSVPGHNDKMQFESSY 120  
DB 251 -LPVKPLESNGALNGEHTVQKKSNSDNL--TPSSELPKRS---RDNNLSRESS-- 302  
QY 121 EGYFLACEKERDLFKLILKKEDELGDRS 148  
DB 303 -----VSSKHLGDNYSRNNYKRRDPDRPT 325

#### RESULT 3

T39487  
hypothetical protein SPBC15D4.11c - fission yeast (Schizosaccharomyces pombe)  
C;Species: Schizosaccharomyces pombe  
C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 04-Mar-2000  
C;Accession: T39487  
R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Lucas, M.; Gaillardin, C.  
submitted to the EMBL Data Library, August 1997  
A;Reference number: Z21858  
A;Accession: T39487  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-263 <LYN>  
A;Cross-references: EMBL:AL031349; PIDN:CAA20486.2; GSPDB:GN00067; SPDB:SPBC15D4.11c  
A;Experimental source: strain 972h-; cosmid cl5D4  
C;Genetics:  
A;Gene: SPDB:SPBC15D4.11c  
A;Map position: 2  
A;Introns: 96/2; 147/3  
C;Superfamily: Schizosaccharomyces pombe hypothetical protein SPBC15D4.11c

Query Match 10.1%; Score 82; DB 2; Length 263;  
Best Local Similarity 21.7%; Pred. No. 2;  
Matches 35; Conservative 33; Mismatches 65; Indels 28; Gaps 5;  
QY 4 KLESKLVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIIISMVKDSQPRGMV 63  
DB 47 KLDSELGIVKQVLDLTPKPKGYEKALHSFIHED-----PSLNYSIALKETAKERIRVT 100  
QY 64 ISVKCEKISXLSKSCNIIISFEMNPPDNIKDTKSDIIFQRSVPGH----- 109  
DB 101 VPVYSSRKSYV--QTKPITHSAEN--ENGNETSDELVFFQHSIPAYVQLTNNHGTILCAL 156  
QY 110 ---DNKMQFESSYGYGYFLACEKERDLFKLILKKEDELGDR 147  
DB 157 ILCKGMLHFDSTFSQSPQNSQAFSSDL-RLILQKSQKTYGR 196

#### RESULT 4

S10532  
interleukin-1 alpha precursor - pig  
A;Alternate names: hematopoietin-1; IL-1 alpha  
C;Species: Sus scrofa domestica (domestic pig)  
C;Date: 20-Feb-1995 #sequence\_revision 22-Nov-1996 #text\_change 28-Jan-2000  
C;Accession: S10532  
R;Maliszewski, C.R.; Renshaw, B.R.; Schoenborn, M.A.; Urban, J.F.; Baker, P.E.  
Nucleic Acids Res. 18, 4282, 1990  
A;Title: Porcine IL-1 alpha cDNA nucleotide sequence.  
A;Reference number: S10532; MUID:90332454; PMID:2377484  
A;Accession: S10532  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-270 <MAL>  
A;Cross-references: EMBL:X52731; NID:g1987; PIDN:CAA36945.1; PID:g1988

C;Comment: Produced by activated macrophages, the IL-1 proteins stimulate thymocyte proliferation.  
C;Comment: IL-1 proteins are involved in the inflammatory response, being identified as ILs.

C;Comment: This protein lacks a conventional signal sequence for protein export. Cleaved form of interleukin-1alpha, unlike interleukin-beta, is fully active.

C;Superfamily: Interleukin-1

C;Keywords: cytokine; immunoregulation; inflammation; lipoprotein; lymphokine; macrophage

F1-112/Domain: propeptide #status predicted <PRO>

F113-270/Product: interleukin-1 alpha #status predicted <ILL>

F182.83/Binding site: myristate (Lys) (covalent) #status predicted

Query Match 10.0%; Score 81.5; DB 1; Length 270;  
Best Local Similarity 22.7%; Pred. No. 2.3;  
Matches 30; Conservative 32; Mismatches 57; Indels 13; Gaps 6;

QY 8 KLSVIRNLNDQVLFIDQGNRPLFEDMTD----SDCRDNAPRTI-FIISMVKDSQPRGMV 62  
DB 123 KYNFMRVINHQCILNDARNQSIIRDPGQYLMAAVLNLDLDEAVKFDMAAYTSNDDSQLPV 182

QY 63 TISVKCEKISXLSKSCN--KIISFKEM-NPPDNIKDTKSDIIFQRSVPGHNDKMQFESS 119  
DB 183 TLIRIS-ETRLVFAQNEDEPVLKELPETPKTIKDETSLLFFWEK----HGNMDYFKSAA 237

QY 120 YEGYFLACEKER 131  
DB 238 HPKLFIATROEK 249

#### RESULT 5

C71509  
probable DNA polymerase I - Chlamydia trachomatis (serotype D, strain UW3/Cx)  
C;Species: Chlamydia trachomatis  
C;Date: 13-Sep-1998 #sequence\_revision 13-Sep-1998 #text\_change 08-Oct-1999  
C;Accession: C71509  
R;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell, Science 282, 754-759, 1998  
A;Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trachomatis serotype D, strain UW-3/Cx  
A;Reference number: A71570; MUID:99000809; PMID:9784136  
A;Accession: C71509  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-866 <ARN>  
A;Cross-references: GB:AE001273; NID:g3328916; PIDN:AAC68093.1; PID:g332892  
A;Experimental source: serotype D, strain UW-3/Cx  
C;Genetics:  
A;Gene: po1A  
C;Superfamily: DNA-directed DNA polymerase I

Query Match 9.9%; Score 80.5; DB 2; Length 866;  
Best Local Similarity 26.4%; Pred. No. 11;  
Matches 34; Conservative 22; Mismatches 28; Indels 45; Gaps 8;  
QY 1 YFGKLESKLVIRNLNDQVLF--DQGNRPLFEDMTD-----SDCRDNAPRTIFII 49  
DB 441 YFGMLASKLLAIKN---YLFVKLEKGLKDIETVEQPLEAVLFAMEC-----V 486

QY 50 SMYKDSQPRGMV---TISVKCEKIS-----XLSKCNKIISFKEMN-----PPDN 91  
DB 487 GMLPDSQ--GLAVLDRLDTKELECSQBIYDLVGCEFNKPKQLSDILYQRLGIEPVDK 544  
QY 92 IKDTKSDII 100  
DB 545 AKSTKAQEV 553

#### RESULT 6

D64583  
hypothetical protein HP0508 - Helicobacter pylori (strain 26695)  
C;Species: Helicobacter pylori  
C;Date: 09-Aug-1997 #sequence\_revision 09-Aug-1997 #text\_change 08-Oct-1999  
C;Accession: D64583  
R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.



C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel  
Nature 403, 665-668, 2000  
A:Title: The genome sequence of the food-borne pathogen *Campylobacter jejuni* reveals hy  
A:Reference number: A81250; MUID:20150912; PMID:10688204  
A:Accession: A81261  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-364 <PAR>  
A:Cross-references: GB:AL139079; GB:AL111168; NID:96968971; PIDN:CAB73631.1; PID:9696906  
A:Experimental source: serotype O2, strain NCTC 11168  
C:Genetics:  
A:Gene: C41643

Query Match	9.5%	Score 77;	DB 2;	Length 364;
Best Local Similarity	24.8%;	Pred. No. 8.9;		
Matches 38;	Conservative 21;	Mismatches 40;	Indels 54;	Gaps 9;
QY	12	IRLNLDQVLFDGGRNRLFEEDMTDSDCRD-NAPRTIFILSMYK----	DSOPR-----	58
Db	211	LRKLINEKILFADRGSTUYFQVLRDN--MDLNISTEVFAKDLKSNLPDSPKPKINFTS	269	
QY	59	--GMAVTISYKCEKI-----	SLXSCENKII--SPKEMPPPNII-----	92
Db	269	NLGITVNASLVVTKIDPKSKVSNAAGFMVGDKILRVNIIILNNFKEL--	QNILSAGNDFS	325
QY	93	-----KDTKSIIFFQFSVPGH-----	DNNMQF	115
Db	326	ILIERKSTKLPLSNFNNEELGANSNGCGDKRFOF	358	

RESULT 11

T00679  
hypothetical protein At2g43990 [imported] - Arabidopsis thaliana  
N:Alternate names: hypothetical protein F6E13.12  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 01-Feb-1999 #sequence\_revision 01-Feb-1999 #text\_change 23-Mar-2001  
C:Accession: T00679; A84873  
R:Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes,  
submitted to the EMBL Data Library, June 1998  
A:Description: Arabidopsis thaliana chromosome II BAC F6E13 genomic sequence.  
A:Reference number: Z14180  
A:Accession: T00679  
A:Status: translated from GB/EMBL/DBDJ  
A:Molecule type: DNA  
A:Residues: 1-632 <ROU>  
A:Cross-references: EMBL:AC004005; NID:g3212846; PID:g3212856  
A:Experimental source: cultivar Columbia  
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;  
cuss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.  
Nature 402, 761-768, 1999  
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A:Reference number: A84420; MUID:20083487; PMID:10617197  
A:Accession: A84873  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-632 <STO>  
A:Cross-references: GB:AE002093; NID:g3212856; PIDN:AAC23407.1; GSPDB:GN00139  
C:Genetics:  
A:Gene: At2g43990; F6E13.12  
A:Map position: 2

	Query Match	9.4%	Score 76	DB 2	Length 632	
	Best Local Similarity	25.6%	Pred. No. 21			
	Matches 34	Conservative 29	Mismatches 40	Indels 30	Gaps 9	
QY	28	PLFEDMTDSD-CRDNAPRTIIISMVKDSQPRGMVATISVKCEK-----ISXLSCEK	79			
DB	368	PLSDRSASSDLCNISSGSSALPMDIYKETTR-----ISSLSPELFRFRRIHLSGDSGE	424			
QY	80	IIISFK-----EMNPDPNIIKTKSDIIFPQRGVP--GHDKMKQF--EBSYSYGYT-LACEK	129			
DB	425	ASAFDTPTCLDSEHLHGDKSSPL-----SVDTLGSENVLOTPESSNSFPNYIQLSCSO	480			

Qy	130	ERDLFKLILKED	142
Db	481	AE-----IOKKHD	488

RESULT 12

E84598  
hypothetical protein At2g29620 [imported] - Arabidopsis thaliana  
C/Species: Arabidopsis thaliana (mouse-ear cress)  
C/Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 02-Feb-2001  
C/Accession: E84698  
R.; Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii,  
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanNaken, S.E.; Umayam, L.; Tal,  
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Ve  
Nature 402, 761-768, 1999  
A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A/Reference number: A84420; MUID:20083487; PMID:10617197  
A/Accession: E84698  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-747 <STC>  
A/Cross-references: GB:AE002093; NID:g3582336; PIDN:AAC35233.1; GSPDB:GN00139  
C/Genetics:  
A/Gene: At2g29620  
A/Map position: 2

```

Query Match      9.4%; Score 76; DB 2; Length 747;
Best Local Similarity 24.7%; Pred. No. 26;
Matches 36; Conservative 29; Mismatches 59; Indels 22; Gaps 7;

Qy      4 KLSKSLVLENLDQVLFDIQGNRPFLFEDMTDSDCRDNAPRTTIFITSMYKDSPRGMAVT 63
       ||| : | | | | | : | | : | | : | | : | | : | | : | | : | | : | |
Db     102 KLHQDSVRNRRKV-----EEVGKWDDSQASEDERGKVLTLLTYGEVLPE---T 150

Qy     64 ISVKCKISXLSCENKIIISKFNPPDNIKDTKSIDIFFOR--SVPGHDKNMQFE----SS 118
       ||| : | | | | | : | | : | | : | | : | | : | | : | | : | | : | |
Db    151 ITPDMKEFK---RERTLLVAEENVFDSVLNDNRDLVELERLISVDG-DDESEVECSSTS 205

Qy    119 SYGYFLACEKERDLPKLILK-KEDE 143

Db   206 SSGEGEEEEERREDVSKVVVAWTEDD 231

```

## RESULT 13

S15661  
(2'-5')oligo(A) synthetase (EC 2.7.7.-) L1 - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C>Date: 31-Dec-1993 #sequence\_revision 02-Jun-1994 #text\_change 16-Jul-1999  
C:Accession: S15661; S19108  
R:Rutherford, M.N.; Kumar, A.; Nissim, A.; Chebath, J.; Williams, B.R.G.  
Nucleic Acids Res. 19, 1917-1924, 1991  
A>Title: The murine 2-5A synthetase locus: three distinct transcripts from two linked genes  
A:Reference number: S15660; MUID:91232962; PMID:1709495  
A:Accession: S15661  
A:Molecule type: mRNA  
A:Residues: 1-192 <RUT>  
A:Cross-references: EMBL:X55982  
R:Williams, B.  
submitted to the EMBL Data Library, September 1990  
A:Reference number: S19108  
A:Accession: S19108  
A:Molecule type: mRNA  
A:Residues: 1-175, 'L', 177-192 <WIL>  
A:Cross-references: EMBL:X55982; NID:g49714; PIDN:CAA39455.1; PID:g49715  
C:Superfamily: oligo(A) synthetase  
C:Keywords: nucleotidyltransferase

Query Match 9.3%; Score 75.5; DB 2; Length 192;  
Best local Similarity 23.2%; Pred. No. 5.8;  
Matches 42; Conservative 24; Mismatches 50; Indels 65; Gaps 9;  
3 GKLESKLSVRN-----LNQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFISMYKD 54

```

Db      11  GRSDADLVFNLLNTSPEDQINQGVLLKEIKQLCEVQHERRC----- 54
QY      55  SQPRGMVAVTSVKCEKISXISCENKIISFKEMNPPDNIKDTKSDII----- 100
Db      55  -----GVKPEVHSLSPNSRALSFK-LSAPDLLKEVKFDVLPAYDLLDHLNLKK 103
QY      101  -----FFQR---SVP-GHDNKMQPFSSSYEGVELACE--KERDLFKLI-----LKKEDELG 145
Db      104  PNOQFYANLISGVPAEGKGLSICFMGLQKLYFLNCRPTKUKRLRLVTHWYQLCKE-KLG 162
QY      146  D 146
Db      163  D 163

RESULT 14
I46620
interleukin-1 alpha precursor - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 04-Feb-2000
C;Accession: I46620
R;Maliszewski, C.
Nucleic Acids Res. 14, 4282, 1990
A;Title: Nucleotide sequence of porcine interleukin-1 alpha.
A;Reference number: I46620
A;Accession: I46620
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-270 <MAL>
A;Cross-references: GB:M86730; NID:g164622; PIDN:AAA73198.1; PID:g164623
C;Superfamily: interleukin-1
C;Keywords: lipoprotein; myristylation
F;1-112/Domain: propeptide #status predicted <PRO>
F;113-270/Product: interleukin-1 alpha #status predicted <ILI>
F;82,83/Binding site: myristate (lys) (covalent) #status predicted

Query Match          9.3%; Score 75.5; DB 2; Length 270;
Best Local Similarity 22.0%; Pred. No. 8.7;
Matches 29; Conservative 32; Mismatches 58; Indels 13; Gaps 6;

QY      8  KLSVIRNLNDQVLFDQGNRPLFEDMTD----SDCRDNAPRTI-FIISMYKDSQPRGMV 62
Db      123  KYNFMRVINHCILINDARNQSIIRDPSQYLMRAVINLDEAVKFDMAAYTSNDDSQLPV 182
QY      63  TISVKCEKISXISCEN--KIISFKEM-NPDDNINKTSDIIFQORSVPGHDNKMQPFSSS 119
Db      183  TLRIS-ETRLFVSAQNEDEPVLKELPPTKTIDETSLFFWEK----HGNMDYFKSAA 237
QY      120  YEGYFLACEKER 131
Db      238  HPKLLIATRQEK 249

RESULT 15
H64245
hypothetical protein MG414 - Mycoplasma genitalium
C;Species: Mycoplasma genitalium
C;Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 02-Mar-2001
C;Accession: H64245; G64245
R;Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.;
M.; Fuhrmann, J.; Nguyen, D.; Utterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, J.
C.A.; Venter, J.C.
Science 270, 397-403, 1995
A;Title: The minimal gene complement of Mycoplasma genitalium.
A;Reference number: A64200; MUID:96026346; PMID:7569993
A;Accession: H64245
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-1036 <TIGR>
A;Cross-references: GB:U39727; GB:I43967; NID:g1046127; PID:g1046128; TIGR:MG414
A;Experimental source: strain G-37
A;Accession: G64245
```

```

A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 'M',310-1036 <TIG2>
A;Cross-references: GB:U39727; GB:I43967; NID:g1046127; PID:g1046128; TIGR:MG413
A;Experimental source: strain G-37
C;Genetics:
A;Genetic code: SGC3
A;Start codon: GTG
C;Superfamily: hypothetical protein MG413

Query Match          9.3%; Score 75.5; DB 2; Length 1036;
Best Local Similarity 21.9%; Pred. No. 43;
Matches 33; Conservative 32; Mismatches 65; Indels 21; Gaps 6;

QY      14  NLNDQVLFDQGNRPLFED--MTDSDCRDNAPRTI-FIISMYKDSQPRGMVAVTSVKCEK- 70
Db      845  SLNDEQLLVKLNITLSEKRLQTTKNVRFNLKNKFINIHLENKQFNVLVFDVDRSKKL 904
QY      71  -ISXISCENKIISFKEMNPPDNIKDTKSDIIFQORSVPGHDNKMQPFSSSYEGYFLACEK 129
Db      905  FIKGVNNDNOVFISY-----DLKITNNQTLIV-DANGFDNSIWFDTIS-----EN 950
QY      130  ERDLFKLI---LKKEDELGDRSIMFTVQNEED 157
Db      951  QTQLFKALSPYLKQNNLQFKRVPDFNLKSQD 981

Search completed: August 19, 2004, 13:36:45
Job time : 17 secs
```





GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 19, 2004, 13:31:14 ; Search time 13 Seconds  
(without alignments)  
628.847 Million cell updates/sec

Title: US-09-716-356A-6

Perfect score: 812  
Sequence: 1 YFGKLESLKSVIRNLNDQVL.....LKKDELGDRSIMFTVQNEED 157

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Match	Query Match Length	ID	Description
1	811	99.9	193	IL18_HUMAN	Q14116 homo sapien
2	659	81.2	193	IL18_HORSE	Q9XSQ7 equus caball
3	654	80.5	193	IL18_BOVIN	Q9TU73 bos taurus
4	637	78.4	192	IL18_PIG	Q19073 sus scrofa
5	633	75.5	193	IL18_CANFA	Q9XS80 canis familiar
6	545	63.4	192	IL18_MOUSE	P70380 mus musculus
7	514.5	63.4	194	IL18_RAT	P97636 rattus norv
8	178.5	22.0	196	IL18_CHICK	Q8QFQ8 gallus gall
9	88	10.8	4705	PAT2_DROME	Q9VW71 drosophila
10	81.5	10.0	270	IL1A_PIG	P18430 sus scrofa
11	81	10.0	267	IL1A_RABIT	P04822 oryctolagus
12	80	9.9	1449	DPO3_CLOPE	Q8XJ33 clostridium
13	79.5	9.8	664	DNAK_CHLCV	Q824B2 chlamydomophi
14	77.5	9.5	674	MUTL_CLOPE	Q8X186 clostridium
15	76.5	9.4	270	IL1A_HORSE	Q28385 equus caball
16	75.5	9.3	192	OASB_MOUSE	Q60856 mus musculus
17	75.5	9.3	1036	Y414_MYCGE	P47653 mycoplasma
18	75.5	9.3	1663	CO3_MOUSE	P01027 mus musculus
19	74.5	9.2	1228	EMI4_HUMAN	Q13201 homo sapien
20	74	9.1	467	M3K8_MOUSE	Q07174 mus musculus
21	74	9.1	467	M3K8_RAT	Q63562 rattus norv
22	74	9.1	1772	MSPI_PLAYO	P13828 plasmodium
23	73	9.0	270	IL1A_FELCA	Q46613 felis silve
24	73	9.0	418	SYS_UREPA	Q9PR38 ureaplasma
25	73	9.0	426	YCXK_ASTLO	P58151 astasia lon
26	72.5	8.9	313	COL4_ARATH	Q9M9B3 arabidopsis
27	72.5	8.9	412	UVSE_CLOPE	Q8XIP3 clostridium
28	71.5	8.8	268	IL1A_BOVIN	P08831 bos taurus
29	71.5	8.8	467	M3K8_HUMAN	P41279 homo sapien
30	71.5	8.8	527	RAG2_HUMAN	P55895 homo sapien
31	71	8.7	700	NONA_DROME	Q04047 drosophila
32	70.5	8.7	245	KDSB_FUSNN	Q8F848 fusobacteri
33	70.5	8.7	268	IL1A_CAPHI	P79161 capra hircu

#### RESULT 1

IL18_HUMAN					
ID	IL18_HUMAN	STANDARD;	PRT;	193 AA.	
AC	Q14116; O75599;				
DT	15-JUL-1998 (Rel. 36, Created)				
DT	15-JUL-1998 (Rel. 36, Last sequence update)				
DT	10-OCT-2003 (Rel. 42, Last annotation update)				
DE	Interleukin-18 precursor (IL-18) (Interferon-gamma inducing factor)				
DE	(IFN-gamma-inducing factor) (Interleukin-1 gamma) (IL-1 gamma).				
GN	IL18 OR IGIF.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
[1]	_TaxID=9606;				
RN	SEQUENCE FROM N.A.				
RP	TISSUE=Liver;				
RC	MEDLINE=96247646; PubMed=8666798;				
RX	Ushio S., Namba M., Okura T., Hattori K., Nukada Y., Akita K.,				
RA	Tanabe F., Konishi K., Micallef M., Fujii M., Torigoe K., Tanimoto T.,				
RA	Fukuda S., Ikeda M., Okamura H., Kurimoto M.;				
RT	"Cloning of the cDNA for human IFN-gamma-inducing factor, expression				
RT	in Escherichia coli, and studies on the biologic activities of the				
RT	protein.";				
RL	J. Immunol. 156:4274-4279(1996).				
[2]					
RN	SEQUENCE FROM N.A.				
RP	Yong D., Guixin D., Lihua H., Haitao W.;				
RA	"Cloning and sequencing of the cDNA for precursor hIL-18.";				
RT	Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.				
[3]					
RN	SEQUENCE FROM N.A.				
RP	Liu J., Peng X., Yuan J., Qiang B.;				
RT	"Cloning of human interleukin 18 cDNA.";				
RL	Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.				
[4]					
RN	SEQUENCE FROM N.A.				
RP	TISSUE=Urinary bladder;				
RX	MEDLINE=22388257; PubMed=12477932;				
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,				
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,				
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,				
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,				
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,				
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,				
RA	Brownstein M.J., Usdan T.B., Toshiyuki S., Carninci P., Prange C.,				
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,				
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,				
RA	Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,				
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.				
RA	Faney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,				
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,				
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,				
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,				
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,				
RA	Schmerch A., Schein J.E., Jones S.J.M., Marra M.A.;				

#### ALIGNMENTS

"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";  
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
[5]  
SEQUENCE OF 2-193 FROM N.A.  
RC TISSUE=Peripheral blood;  
RA Conti B., Kim S.J., Tinti C., Chun H.S., Joh T.H.;  
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS  
CC AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I  
CC CELLS.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: Belongs to the IL-1 family.  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; D49550; BA08706.1; -.  
CC EMBL; AF077611; AAC27787.1; -.  
CC EMBL; AY044641; AAK35950.1; -.  
CC EMBL; BC007007; AAH07007.1; -.  
CC EMBL; BC007461; AAH07461.1; -.  
CC EMBL; U90434; AAB50010.1; -.  
CC Genew; HGNC:5986; IL18.  
CC MIW; 600953; -.  
CC GO; GO:0005576; C:extracellular; TAS.  
CC GO; GO:0016506; F:apoptosis activator activity; ISS.  
CC GO; GO:0005125; F:cytokine activity; TAS.  
CC GO; GO:0004871; F:signal transducer activity; TAS.  
CC GO; GO:0001525; P:angiogenesis; IDA.  
CC GO; GO:0007267; P:cell-cell signaling; TAS.  
CC GO; GO:0042033; P:chemokine biosynthesis; TAS.  
CC GO; GO:0042253; P:granulocyte macrophage colony-stimulating f. . .; TAS.  
CC GO; GO:0006955; P:immune response; TAS.  
CC GO; GO:0008625; P:induction of apoptosis via death domain rec. . .; ISS.  
CC GO; GO:0042095; P:interferon-gamma biosynthesis; TAS.  
CC GO; GO:0042231; P:interleukin-2 biosynthesis; TAS.  
CC GO; GO:0042094; P:interleukin-2 biosynthesis; TAS.  
CC GO; GO:0042104; P:positive regulation of activated T-cell pro. . .; IDA.  
CC GO; GO:0030155; P:regulation of cell adhesion; IDA.  
CC GO; GO:0030431; P:sleep; ISS.  
CC GO; GO:0042032; P:T-helper 2 type immune response; TAS.  
CC InterPro; IPR008996; Cytok\_IL1\_like.  
CC InterPro; IPR000975; Interleukin\_1.  
CC SMART; SM00125; IL1; 1.  
CC Cytokine.  
KW PROPEP 1 36 BY SIMILARITY.  
FT CHAIN 37 193 INTERLEUKIN-18.  
FT CONFLICT 66 66 F -> L (IN REF. 2).  
FT CONFLICT 86 86 S -> R (IN REF. 2).  
FT CONFLICT 191 191 N -> S (IN REF. 2).  
SQ SEQUENCE 193 AA; 22326 MW; 323C62C203788D55 CRC64;  
Query Match 99.9%; Score 811; DB 1; Length 193;  
Best Local Similarity 99.4%; Pred. No. 1.3e-68;  
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTFIISMYKDSQPRGM 60  
Db 37 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTFIISMYKDSQPRGM 96  
Qy 61 AVTISVKCEKLSXLSCKENKIISFKEMPPDNKDKSDIIFQFQSVFGHDKMQFESSY 120  
Db 97 AVTISVKCEKISTLSCKENKIISFKEMPPDNKDKSDIIFQFQSVFGHDKMQFESSY 156  
Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157  
Db 157 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 193  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

RESULT 2  
IL18 HORSE  
ID IL18 HORSE STANDARD; PRT; 193 AA.  
AC Q9XSQ7;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Interleukin-18 precursor (IL-18) (Interleukin-gamma inducing factor)  
DE (IFN-gamma-inducing factor) (Interleukin-1 gamma) (IL-1 gamma).  
GN IL18 OR IGIF.  
OS Equus caballus (Horse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
OX NCBI\_TaxID=9796;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Nicolson L., Penha-Goncalves M.N., Keanie J.L., Logan N.A.,  
RA Argyle D.J., Onions D.E.;  
RL "Nucleotide sequence of equine interleukin 12 and 18 cDNAs.";  
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS  
CC AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I  
CC CELLS (BY SIMILARITY).  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: Belongs to the IL-1 family.  
CC  
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CC  
CC EMBL; Y11131; CA722013.1; -.  
CC InterPro; IPR008996; Cytok\_IL1\_like.  
KW Cytokine.  
FT PROPEP 1 36 BY SIMILARITY.  
FT CHAIN 37 193 INTERLEUKIN-18.  
SQ SEQUENCE 193 AA; 22058 MW; 4D81535E9004ECAP CRC64;  
Query Match 81.2%; Score 659; DB 1; Length 193;  
Best Local Similarity 77.7%; Pred. No. 1.8e-54;  
Matches 122; Conservative 21; Mismatches 14; Indels 0; Gaps 0;  
Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTFIISMYKDSQPRGM 60  
Db 37 YFGKLEPKLSIIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTFIISMYKDSLTRGL 96  
Qy 61 AVTISVKCEKLSXLSCKENKIISFKEMPPDNKDKSDIIFQFQSVFGHDKMQFESSY 120  
Db 97 AVTISVKCEKISTLSCKENKIISFKEMPPDNKDKSDIIFQFQSVFGHDKMQFESSY 156  
Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157  
Db 157 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 193  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

RESULT 3  
IL18 BOVIN  
ID IL18 BOVIN STANDARD; PRT; 193 AA.  
AC Q9TU73;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Interleukin-18 precursor (IL-18) (Interleukin-gamma inducing factor)  
DE (IFN-gamma-inducing factor) (Interleukin-1 gamma) (IL-1 gamma).  
GN IL18.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

```

CC Bovidae; Bovinae; Bos.
CC NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20012648; PubMed=10547157;
RA Shoda L.K., Zarlega D.S., Hirano A., Brown W.C.;
RT "Cloning of a cDNA encoding bovine interleukin-18 and analysis of IL-
RT 18 expression in macrophages and its IFN-gamma-inducing activity.";
RL J. Interferon Cytokine Res. 19:1169-1177(1999).
CC -!- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
CC AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I
CC CELLS (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the IL-1 family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: AF124789; AAF08686.1; -.
CC InterPro: IPR008996; Cytok IL1 like.
CC SMART; SM00125; IL1; 1.
CC CHAIN 37 193
CC PROPEP 1 36 BY SIMILARITY.
CC CYTOKINE.
CC FT CHAIN 37 193 INTERLEUKIN-18.
CC FT PROPEP 1 36 BY SIMILARITY.
CC FT CHAIN 37 193 INTERLEUKIN-18.
CC SQ SEQUENCE 193 AA; 22347 MW; 65720F199DEA49C4 CRC64;

Query Match 80.5%; Score 654; DB 1; Length 193;
Best Local Similarity 77.1%; Pred. No. 5.4e-54;
Matches 121; Conservative 23; Mismatches 13; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDVLFIDQGNRPFLFEDMTSDCRNAPRTIFIISMYKDSQPRGM 60
DB 37 HFGLKPKLSIIRNLNDVLFINQGVQVFPEDPDSDCSDNAPQTIFLIYMYKDSLTRL 96
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 AVTISVCKEKISLSCENKIISFKENPPDNIDKTSDIIFQSVPGHDKMKQFESSY 120
DB 97 AVTISVQCKKMTSLSCNKNTLSFKENPPDNIDNEESDIIFQSVPGHDKKQFESSLY 156
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
121 EGYFLACEKERDLFKLILKKEBELGDRSINFTVQNE 157
DB 157 KGYFLACKENDLFKLILKKQDDNRDKSVNFTVQNN 193
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 4
IL18_PIG
ID IL18_PIG STANDARD; PRT; 192 AA.
AC O19073;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Interleukin-18 precursor (IL-18) (interferon-gamma inducing factor)
DE (IFN-gamma-inducing factor) (interleukin-1 gamma) (IL-1 gamma).
GN IL18 OR IGIF.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
CC NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Foss D.L., Murtaugh M.P.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Penha-Goncalves M.N., Logan N.A., Nicolson L., Onions D.E.;
RA Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.

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RA Muneta Y., Mori Y.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=20260994; PubMed=10803849;
RA Fournout S., Dozois C.M., Yerle M., Pinton P., Fairbrother J.M.,
RA Oswald E., Oswald I.P.;
RT "Cloning, chromosomal location, and tissue expression of the gene for
RT pig interleukin-18.";
RL Immunogenetics 51:358-365(2000).
CC -!- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
CC AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I
CC CELLS (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the IL-1 family.
CC
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CC
CC EMBL: U68701; AAC18415.1; -.
CC EMBL: Y11132; CAA72014.1; -.
CC EMBL: AB010003; BAA24135.1; -.
CC EMBL: AF191088; AAF71200.1; -.
CC GO: GO:0005576; C:extracellular; ISS.
CC GO: GO:0001525; P:cytokine activity; IMP.
CC GO: GO:0042033; P:chemokine biosynthesis; ISS.
CC GO: GO:0008625; P:induction of apoptosis via death domain rec. .; IDA.
CC GO: GO:0042095; P:interferon-gamma biosynthesis; IDA.
CC GO: GO:0042104; P:positive regulation of activated T-cell pro. .; ISS.
CC GO: GO:0008284; P:positive regulation of cell proliferation; IDA.
CC InterPro: IPR008996; Cytok IL1 like.
CC InterPro: IPR000975; Interleukin_1.
CC SMART; SM00125; IL1; 1.
CC CYTOKINE.
CC FT PROPEP 1 35 BY SIMILARITY.
CC FT CHAIN 36 192 INTERLEUKIN-18.
CC SQ SEQUENCE 192 AA; 22026 MW; 881EA654E221A17A CRC64;

Query Match 78.4%; Score 637; DB 1; Length 192;
Best Local Similarity 75.2%; Pred. No. 2e-52;
Matches 118; Conservative 24; Mismatches 15; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDVLFIDQGNRPFLFEDMTSDCRNAPRTIFIISMYKDSQPRGM 60
DB 36 YFGKLEPKLSIIRNLNDVLFINQGVQVFPEDPDSDCSDNAPQTIFLIYMYKDSLTRL 95
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 AVTISVCKEKISLSCENKIISFKENPPDNIDKTSDIIFQSVPGHDKMKQFESSY 120
DB 96 AVTISVQCKKMTSLSCNKNTLSFKENPPDNIDNEGDNIIFQSVPGHDKKQFESSLY 155
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
121 EGYFLACEKERDLFKLILKKEBELGDRSINFTVQNE 157
DB 156 KGYFLACKENDLFKLILKKECDGDKSINFTVQNN 192
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 5
IL18_CANFA
ID IL18_CANFA STANDARD; PRT; 193 AA.
AC Q9XSR0;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Interleukin-18 precursor (IL-18) (interferon-gamma inducing factor)
DE (IFN-gamma-inducing factor) (interleukin-1 gamma) (IL-1 gamma).
GN IL18 OR IGIF.
OS Canis familiaris (Dog).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=99309818; PubMed=10380699;
RA Argyle D.J., McGillivray C., Nicolson L., Onions D.E.;
RT "Cloning, sequencing, and characterization of dog interleukin-18.";
RL Immunogenetics 49:541-543(1999).
CC -!- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
CC AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I
CC CELLS (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the IL-1 family.
CC
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CC or send an email to license@isb-sib.ch).
CC
DR EMBL; Y11133; CAA72015.1; -.
DR GO; GO:0005576; C:extracellular; TAS.
DR GO; GO:0016506; F:apoptosis activator activity; ISP.
DR GO; GO:0005125; F:cytokine activity; TAS.
DR GO; GO:0042033; P:chemokine biosynthesis; ISS.
DR GO; GO:0008625; P:induction of apoptosis via death domain rec. .; ISP.
DR GO; GO:0042035; P:interferon-gamma biosynthesis; IDA.
DR GO; GO:0042104; P:positive regulation of activated T-cell pro. .; ISS.
DR InterPro; IPR008996; Cytok_IL1_like.
KW Cytokine.
FT PROPEP 1 36 BY SIMILARITY.
FT CHAIN 37 193 INTERLEUKIN-18.
FT SEQUENCE 193 AA; 22037 MW; 0D973E586F461F25 CRC64;
Query Match 75.5%; Score 613; DB 1; Length 193;
Best Local Similarity 73.7%; Pred. No. 3.5e-50;
Matches 115; Conservative 23; Mismatches 18; Indels 0; Gaps 0;
QY 1 YFGKLEKSLVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMKYDSQPRGM 60
DB 37 YFGKLEKSLVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMKYDSQPRGM 96
QY 61 AVTISVKCEKISLSCENKILSFEMPPDNKTKSDIIFQSVPGHDKMOPFESSY 120
DB 97 AVTISVKYKNTSLSCNKNTLSFQMSPPDSINDEGNDIIFQSVPGHDDKIQFESSLY 156
QY 121 EGYFLACEKERDLFKLLKKEDELDGDSIMFTVQNE 156
DB 157 KGHEFLACKENDLPKLLKDKDENGDKSIMFTVQNK 192
RESULT 6
IL18 MOUSE STANDARD; PRT; 192 AA.
AC P70380;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Interleukin-18 precursor (IL-18) (interferon-gamma inducing factor)
DE (IFN-gamma-inducing factor) (interleukin-1 gamma) (IL-1 gamma).
GN IL18 OR IGIF.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN (1)
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX TISSUE=Liver;
RC MEDLINE=96061009; PubMed=7477296;
RA Okamura H., Tsutsumi H., Komatsu T., Yutsudo M., Hakura A.,

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RA Tanimoto T., Torigoe K., Okura T., Mukada Y., Hattori K.,
RA Akita K., Namba M., Tanabe F., Konishi K., Fukuda S., Kurimoto M.;
RT "Cloning of a new cytokine that induces IFN-gamma production by T
RT cells.";
RN Nature 378:88-91(1995).
RL (2)
RP SEQUENCE OF 1-191 FROM N.A.
RX STRAIN=NOD; TISSUE=Pancreas;
RX MEDLINE=97174346; PubMed=9022080;
RA Rothe H., Jenkins N.A., Copeland N.G., Kolb H.;
RT "Active stage of autoimmune diabetes is associated with the
RT expression of a novel cytokine, IGIF, which is located near Idd2.";
RL J. Clin. Invest. 99:469-474(1997).
CC -!- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
CC AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I
CC CELLS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the IL-1 family.
CC
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CC
DR EMBL; D49949; BAA08705.1; -.
DR EMBL; U66244; AAB49753.1; -.
DR PIR; S60226; S60226.
DR MGD; MGI:107936; IL18.
DR GO; GO:0005576; C:extracellular; ISS.
DR GO; GO:0016506; F:apoptosis activator activity; TAS.
DR GO; GO:0005125; F:cytokine activity; ISS.
DR GO; GO:0001525; P:angiogenesis; ISS.
DR GO; GO:0042033; P:chemokine biosynthesis; ISS.
DR GO; GO:0042253; P:granulocyte macrophage colony-stimulating f. .; ISS.
DR GO; GO:0008625; P:induction of apoptosis via death domain rec. .; TAS.
DR GO; GO:0042035; P:interferon-gamma biosynthesis; IMP.
DR GO; GO:0042231; P:interleukin-13 biosynthesis; TAS.
DR GO; GO:0042094; P:interleukin-2 biosynthesis; ISS.
DR GO; GO:0042104; P:positive regulation of activated T-cell pro. .; ISS.
DR GO; GO:0030155; P:regulation of cell adhesion; ISS.
DR GO; GO:0030431; P:sleep; ISS.
DR InterPro; IPR008996; Cytok_IL1_like.
DR InterPro; IPR009075; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR SMART; SM00125; IL1; 1.
KW Cytokine.
FT PROPEP 1 35
FT CHAIN 36 192 INTERLEUKIN-18.
FT CONFLICT 183 185 MFT -> IS (IN REF. 2).
SQ SEQUENCE 192 AA; 22135 MW; 8FED938473874D63 CRC64;
Query Match 63.4%; Score 515; DB 1; Length 192;
Best Local Similarity 64.9%; Pred. No. 4.7e-41;
Matches 100; Conservative 27; Mismatches 25; Indels 2; Gaps 2;
QY 2 FGKLEKSLVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMKYDSQPRGMA 61
DB 37 FGRLLHCTTAVIRNLNDQVLFVDK-RQVFEDMTDIDQASASEPQTRLLIYMYKDSVVRGLA 95
QY 62 VTISVKCEKISLSCENKILSFEMPPDNKTKSDIIFQSVPGHDKMOPFESSY 121
DB 96 VTISVKDSRMTSLSCNKILSFEMDPENIDDIQSDLIFFQKRVPGH-NRMEFESSLYE 154
QY 122 GYFLACEKERDLFKLLKKEDELDGDSIMFTVQNE 155
DB 155 GHFLACQKEDDAFKLLKDKDENGDKSVMTFLIN 188
RESULT 7
IL18 RAT

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ID IL18 RAT STANDARD; PRT; 194 AA.  
AC P97636; O88749; P97637;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DE 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Interleukin-18 precursor (IL-18) (Interferon-gamma inducing factor)  
DE (IFN-gamma-inducing factor) (Interleukin-1 gamma) (IL-1 gamma).  
GN IL18 OR IGIF.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RN SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).  
RC STRAIN=Sprague-Dawley; TISSUE=Adrenal gland;  
RX MEDLINE=97152963; PubMed=8998986;  
RA Culhane A.C., Hall M.D., Rothwell N.J., Lusheshi G.N.;  
RT "Cloning of rat brain interleukin-18 cDNA.";  
RL Mol. Psych. 3:362-366(1998).  
CC -1- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS  
CC AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I  
CC CELLS.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=2;  
CC Name=Beta;  
CC Name=Alpha;  
CC IsoId=P97636-1; Sequence=Displayed;  
CC IsoId=P97636-2; Sequence=VSP\_002659;  
CC -1- SIMILARITY: Belongs to the IL-1 family.  
CC -----  
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CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/  
CC or send an email to license@isb-sib.ch).  
CC -----  
CC EMBL; U77776; AAC53009.1; -;  
CC EMBL; U77777; AAC53010.1; -;  
CC EMBL; AJ222813; CAA11001.1; -;  
CC GO; GO:0005576; C:extracellular; ISS.  
CC GO; GO:0016506; F:apoptosis activator activity; ISS.  
CC GO; GO:0005125; F:cytokine activity; ISS.  
CC GO; GO:0005125; P:angiogenesis; ISS.  
CC GO; GO:0008625; P:induction of apoptosis via death domain rec. .; ISS.  
CC GO; GO:0042095; P:interferon-gamma biosynthesis; ISS.  
CC GO; GO:0042104; P:positive regulation of activated T-cell pro. .; ISS.  
CC GO; GO:0030104; P:regulation of cell adhesion; ISS.  
CC GO; GO:0045188; P:regulation of non-REM sleep; TAS.  
CC GO; GO:0030431; P:sleep; IDA.  
CC InterPro; IPR008996; Cytok IL1 like.  
CC Pfam; PF00340; IL1; 1.  
CC SMART; SM00125; IL1; 1.  
CC Cytokine; Alternative splicing.  
CC PROPEP 1 36  
CC CHAIN 37 194  
CC VARSPLIC 121 139  
CC Missing (in isoform Alpha).  
CC /FtId=VSP\_002659.  
CC CONFLICT 4 5  
CC CONFLICT 48 48 MS -> IP (IN REF. 2).  
CC CONFLICT 1 1 I -> M (IN REF. 2).  
CC SEQUENCE 194 AA; 22303 MW; E2089AD6F1798450 CRC64;

Query Match 63.4%; Score 514.5; DB 1; Length 194;  
Best Local Similarity 63.2%; Pred. No. 5.3e-41;  
Matches 98; Conservative 28; Mismatches 28; Indels 1; Gaps 1;  
QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLPFDMDTSDCRDNPARTIFTIISMYKDSQPRGM 60  
DB 37 HFGRLHCTTAVIRSLNDQVLFVDKRNPFVDFMDPDIDRTANESQTRLLIYYMKDSEVKGL 96  
QY 61 AVTISVKEKISXLSKCNKIISFKEMPPDNKIDTKSDIIFQFORSVPGHDKMKOFESSY 120  
DB 97 AVTISVKEKISXLSKCNKIISFKEMPPDNKIDTKSDIIFQFORSVPGHDKMKOFESSY 155  
QY 121 EGVFLACEKEDLFLKLLKKEDELGDRSIMFTVQN 155  
DB 156 EGVFLACEKEDLFLKLLKKEDELGDRSIMFTVQN 190  
RESULT 8  
IL18 CHICK  
ID IL18 CHICK STANDARD; PRT; 196 AA.  
AC Q8QFQ8;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DE 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Interleukin-18 precursor (IL-18).  
GN IL18.  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RN SEQUENCE FROM N.A.  
RA Rothwell L., Buerstedde J.M., Kaiser P.;  
RT "Cloning and characterisation of chicken interleukin-18.";  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS  
CC AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I  
CC CELLS (By similarity).  
CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).  
CC -1- SIMILARITY: Belongs to the IL-1 family.  
CC -----  
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/  
CC or send an email to license@isb-sib.ch).  
CC -----  
CC EMBL; AJ276025; CAC81652.1; -;  
CC InterPro; IPR008996; Cytok IL1 like.  
CC PROPEP 1 29  
CC CHAIN 30 196  
CC SEQUENCE 196 AA; 22787 MW; 4947DECCB92414 CRC64;  
QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLPFDMDTSDCRDNPARTIFTIISMYKDSQPRGM 60  
DB 20 YFELECDAPCKDKTKIRFRFNVNSQLVVRPLNVAFAFEDVTDQEVKGS-GMYFDIHC 78  
QY 52 YKDSQPRG-MAYTISVKCEKISXLSKCNK-----IISFKEMPPDNKIDTKSDIIFQFORS 105  
DB 79 YKTAPSARMPVAFSVQVEDKSYMCCEKHGKMVVRFEQGVPKDIPG-ESNIIFFKKT 137  
QY 106 VPGHDKN-MQFESSSYEGYFLACEKERDLFLKLLKKEDELGDRSIMFTVQN 156  
DB 138 FTSCSKAFKFEYSLEQGMFLAFEEEDSLRKLKLLKKEDELGDRSIMFTVQN 192

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RESULT 9
FAT2_DROME
ID FAT2_DROME STANDARD; PRT; 4705 AA.
AC Q9VM71; Q95S51;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Putative fat-like cadherin-related tumor suppressor homolog
DE precursor.
GN FAT2 OR CG7749.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RX MEDLINE=22426066; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brannon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Glöckner A., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Flosser C., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kianos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [2]
RP REVISIONS.
RX MEDLINE=22426069; PubMed=12537572;
RA Mitra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.N., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review.";
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
RN [3]
RP SEQUENCE OF 3837-4705 FROM N.A.

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RC STRAIN=Berkeley; TISSUE=Ovary;
RX MEDLINE=22426066; PubMed=12537569;
RA Stapleton M., Carlson J.W., Brokstein P., Yu C., Champe M.,
RA George R.A., Guarin H., Krommiller B., Pacleb J.M., Park S., Wan K.H.,
RA Rubin G.M., Celniker S.E.;
RT "A Drosophila full-length cDNA resource.";
RL Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8(2002).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC -!- SIMILARITY: Contains 34 cadherin domains.
CC -!- SIMILARITY: Contains 5 EGF-like domains.
CC -!- SIMILARITY: Contains 1 laminin G-like domain.
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CC -----
CC EMBL; AE003515; AAF49078.2; -;
CC EMBL; AY060955; AAL28503.1; ALT_INIT.
CC EMBL; AY118666; AAM50035.1; ALT_INIT.
CC HSP; P15116; INCI.
CC FlyBase; FBgn0036930; fat2.
CC GO; GO:0005887; C:integral to plasma membrane; ISS.
CC GO; GO:0008014; F:calcium-dependent cell adhesion molecule ac.; ISS.
CC GO; GO:0016339; P:calcium-dependent cell-cell adhesion; ISS.
CC InterPro; IPR000152; ASX_hydroxyl_S.
CC InterPro; IPR002126; Cadherin.
CC InterPro; IPR008985; Cona-like_leg_gf.
CC InterPro; IPR001881; EGF_Ca.
CC InterPro; IPR006209; EGF-like.
CC InterPro; IPR006210; IEGF.
CC InterPro; IPR001791; Laminin_G.
CC Pfam; PF000028; cadherin; 31.
CC Pfam; PF00008; EGF; 5.
CC Pfam; PF00054; laminin G; 1.
CC PRINTS; PR00205; CADHERIN.
CC SMART; SM00112; CA; 34.
CC SMART; SM00181; EGF; 6.
CC SMART; SM00282; LamG; 1.
CC PROSITE; PS00010; ASX HYDROXYL; 1.
CC PROSITE; PS00232; CADHERIN 1; 18.
CC PROSITE; PS00268; CADHERIN 2; 34.
CC PROSITE; PS00022; EGF 1; 5.
CC PROSITE; PS01186; EGF 2; 2.
CC PROSITE; PS00026; EGF 3; 5.
CC PROSITE; PS01187; EGF CA; 1.
CC PROSITE; PS00025; LAM G DOMAIN; 1.
KW Hypothetical protein; Cell adhesion; Signal; Glycoprotein;
KW Transmembrane; Calcium; Calcium-binding; Repeat; EGF-like domain.
FT SIGNAL 1 35
FT CHAIN 36 4705
FT PUTATIVE FAT-LIKE CADHERIN-RELATED TUMOR
FT SUPPRESSOR HOMOLOG.
FT EXTRACELLULAR (POTENTIAL).
FT CYTOPLASMIC (POTENTIAL).
FT CADHERIN 1.
FT CADHERIN 2.
FT CADHERIN 3.
FT CADHERIN 4.
FT CADHERIN 5.
FT CADHERIN 6.
FT CADHERIN 7.
FT CADHERIN 8.
FT CADHERIN 9.
FT CADHERIN 10.
FT CADHERIN 11.
FT CADHERIN 12.
FT CADHERIN 13.
FT CADHERIN 14.
FT CADHERIN 15.

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FT DOMAIN 1715 1812 CADHERIN 16.
FT DOMAIN 1813 1929 CADHERIN 17.
FT DOMAIN 1930 2037 CADHERIN 18.
FT DOMAIN 2031 2137 CADHERIN 19.
FT DOMAIN 2138 2238 CADHERIN 20.
FT DOMAIN 2239 2338 CADHERIN 21.
FT DOMAIN 2339 2465 CADHERIN 22.
FT DOMAIN 2466 2567 CADHERIN 23.
FT DOMAIN 2568 2670 CADHERIN 24.
FT DOMAIN 2671 2779 CADHERIN 25.
FT DOMAIN 2780 2876 CADHERIN 26.
FT DOMAIN 2877 2983 CADHERIN 27.
FT DOMAIN 2984 3088 CADHERIN 28.
FT DOMAIN 3084 3185 CADHERIN 29.
FT DOMAIN 3186 3289 CADHERIN 30.
FT DOMAIN 3290 3394 CADHERIN 31.
FT DOMAIN 3395 3499 CADHERIN 32.
FT DOMAIN 3500 3604 CADHERIN 33.
FT DOMAIN 3605 3712 CADHERIN 34.
FT DOMAIN 3819 3879 EGF-LIKE 1.
FT DOMAIN 3881 3919 EGF-LIKE 2.
FT DOMAIN 3937 4121 LAMININ G-LIKE.
FT DOMAIN 4129 4166 EGF-LIKE 3.
FT DOMAIN 4168 4205 EGF-LIKE 4.
FT DOMAIN 4243 4279 EGF-LIKE 5.
FT DISULFID 3823 3835 POTENTIAL.
FT DISULFID 3830 3867 POTENTIAL.
FT DISULFID 3869 3878 POTENTIAL.
FT DISULFID 3885 3896 POTENTIAL.
FT DISULFID 3890 3907 POTENTIAL.
FT DISULFID 3909 3918 POTENTIAL.
FT DISULFID 4133 4144 POTENTIAL.
FT DISULFID 4138 4154 POTENTIAL.
FT DISULFID 4156 4165 POTENTIAL.
FT DISULFID 4172 4183 POTENTIAL.
FT DISULFID 4177 4193 POTENTIAL.
FT DISULFID 4195 4204 POTENTIAL.
FT DISULFID 4247 4258 POTENTIAL.
FT DISULFID 4252 4267 POTENTIAL.
FT DISULFID 4269 4278 POTENTIAL.
FT CARBOHYD 65 65 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 156 156 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 364 364 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 779 779 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 843 843 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 923 923 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1106 1106 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1198 1198 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1312 1312 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1439 1439 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1473 1473 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1511 1511 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CONFLICT 3962 3962 G -> E (IN REF. 3; AAL28503).
SQ SEQUENCE 4705 AA; 524564 MW; 6D387A489D2C33DE CRC64;

Query Match
Best Local Similarity 10.8%; Score 88; DB 1; Length 4705;
Matches 38; Conservative 25; Mismatches 56; Indels 42; Gaps 7;

QY 32 DMTDSDCRDNAPRTIFITISMY---KDSQPRGMATVTSVKCEKISLSCENKIISF--KE 85
Db 2124 DISVLVDNDCP--LFVNMPPYATVSDIDDPKG---TIIIMQKALDLSAENGVEYELKK 2178
QY 86 MNPDPNITKDTSDIIFQRSVPGHDKMKQFESSYEGYFLACEKERDL----- 133
Db 2179 NGNELFKLDRKSGELSIKQHVGEHNRNVELTVAAYDGAITPCSSEAPLQVKVIDRSMPEV 2238
QY 134 ---FKLILKED-----ELGDRSTMFTVQNE 156
Db 2239 EKQFYTVSVKEDVEMYGALSIVSIEAESPLG-RSLIYTISSSE 2278

RESULT 10

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IL1A_PIG
ID IL1A_PIG STANDARD; PRT; 270 AA.
AC P18430;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Interleukin-1 alpha precursor (IL-1 alpha).
GN IL1A.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=90332454; PubMed=2377484;
RA Maliszewski C.R., Renshaw B.R., Schoenborn M.A., Urban J.F.,
RA Baker P.E.;
RT "Porcine IL-1 alpha cDNA nucleotide sequence.";
RL Nucleic Acids Res. 18:4282-4282(1990).
[2]
RP SEQUENCE FROM N.A.
RA Huether M.J., Scamurra R.W., Murtaugh M.P., Molitor T.W.;
RL Submitted (XXX-1992) to the EMBL/GenBank/DBJ databases.
CC -I- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
CC THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE. B-CELL
CC MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
CC IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
CC IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE
CC THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.
CC -I- SUBUNIT: Monomer.
CC -I- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
CC AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
CC -I- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
CC PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
CC OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
CC SECRETORY PROTEINS.
CC -I- SIMILARITY: Belongs to the IL-1 family.
-----
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CC or send an email to license@isb-sib.ch).
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DR EMBL; X52731; CAA36945.1; -.
DR EMBL; M86730; AAA73198.1; -.
DR PIR; I46620; I46620.
DR PIR; S10532; S10532.
DR HSPP; P01583; IITA.
DR InterPro; IPR008996; Cytok IL1 like.
DR InterPro; IPR003502; IL1_propep.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR Pfam; PF02394; IL1_propep; 1.
DR SMART; SM00125; IL1; 1.
DR PROSITE; PS00253; INTERLEUKIN 1; 1.
DR Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen.
FT PROPEP 1 112
FT CHAIN 113 270 INTERLEUKIN-1 ALPHA.
FT CARBOHYD 102 102 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 141 141 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CONFLICT 89 89 N -> I (IN REF. 2).
FT CONFLICT 242 242 F -> L (IN REF. 2).
FT CONFLICT 255 255 P -> R (IN REF. 2).
SQ SEQUENCE 270 AA; 30788 MW; 5677BF2B0EF63839 CRC64;

Query Match
Best Local Similarity 10.0%; Score 81.5; DB 1; Length 270;
Matches 30; Conservative 32; Mismatches 57; Indels 13; Gaps 6;

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Best Local Similarity 22.3%; Pred. No. 5;  
Matches 29; Conservative 28; Mismatches 62; Indels 11; Gaps 4;  
QY 7 SKLSVIRNLNDQVLFIDQGNRPLFEDMTDSCRDNPRTI-----FIISMVYKDSQPRGWA 61  
Db 122 TKYNFMRIVNHQCTINDALNOSVIRDTSGQVLAATLNNLDDAVKFDMGAYTSEDSQLP 181  
QY 62 VTISV-KCEKISXLSCEKNIISFKEM-NPPDNIKDTKSDIIFQFQSVFPHDNKMQFESS 119  
Db 182 VTLRISKTRLFVSAQNEDEPVLKEMPTPKTIKDTNLLFFWER-----HGSKNYFKSVA 237  
QY 120 YEGYFLACEK 129  
Db 238 HPKLFIAATKQ 247  
Search completed: August 19, 2004, 13:35:28  
Job time : 14 secs

606 ETVEVKYINKIASMSCRAAVKANDVLSDILEMENLIEDLRYINDPFCRGRPTIIFK 661

RESULT 15  
IL1A\_HORSE  
ID IL1A\_HORSE STANDARD; PRT; 270 AA.  
AC Q28385; 077743;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE Interleukin-1 alpha precursor (IL-1 alpha).  
GN IL1A.  
OS Equus caballus (Horse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
OX NCBI\_TaxID=9796;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96131982; PubMed=8578682;  
RA Kato H., Ohashi T., Nakamura N., Nishimura Y., Watari T., Goitsuka R.,  
RA Tsujimoto H., Hasegawa A.;  
RT "Molecular cloning of equine interleukin-1 alpha and -beta cDNAs.";  
RL Vet. Immunol. Immunopathol. 48:221-231(1995).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98285941; PubMed=9622738;  
RA Howard R.D., McIlwraith C.W., Trotter G.W., Nyborg J.K.;  
RT "Cloning of equine interleukin-1 alpha and equine interleukin-1 beta  
and determination of their full-length cDNA sequences.";  
RL Am. J. Vet. Res. 59:704-711(1998).  
CC -!- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES  
CC THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL  
CC MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.  
CC IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING  
CC IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE  
CC THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS  
CC (BY SIMILARITY).  
CC -!- SUBUNIT: Monomer (By similarity).  
CC -!- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE  
CC AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.  
CC -!- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE  
CC PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS  
CC OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER  
CC SECRETORY PROTEINS.  
CC -!- SIMILARITY: Belongs to the IL-1 family.  
CC -----  
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CC -----  
CC EMBL; D42146; BAA07717.1; -;  
CC EMBL; U92480; AAC39255.1; -;  
CC HSP; P01583; LITA.  
CC InterPro; IPR008996; Cytok\_III\_like.  
CC InterPro; IPR003502; IL1\_propep.  
CC InterPro; IPR000975; Interleukin\_1.  
CC Pfam; PF00340; IL1; 1.  
CC Pfam; PF02394; IL1\_propep; 1.  
CC SMART; SM00125; IL1; 1.  
CC PROSITE; PS00253; INTERLEUKIN\_1; 1.  
KW Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen.  
FT PROPEP 1 112 BY SIMILARITY.  
FT CHAIN 113 270 INTERLEUKIN-1 ALPHA.  
FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CONFLICT 110 110 R -> K (IN REF. 2).  
FT CONFLICT 150 150 G -> V (IN REF. 2).  
SQ SEQUENCE 270 AA; 30806 MW; 381859713754DE90 CRC64;

Query Match . 9.4%; Score 76.5; DB 1; Length 270;

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 19, 2004, 13:32:15 ; Search time 39 Seconds

(without alignments)  
1270.163 Million cell updates/sec

Title: US-09-716-356A-6

Perfect score: 812

Sequence: 1 YFGKLSKLSVIRNLNDQVL.....LKKDELGDRSIMFTVQNE 157

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:\*

1: sp\_archaea:\*

2: sp\_bacteria:\*

3: sp\_fungi:\*

4: sp\_human:\*

5: sp\_invertebrate:\*

6: sp\_mammal:\*

7: sp\_mhc:\*

8: sp\_organelle:\*

9: sp\_phase:\*

10: sp\_plant:\*

11: sp\_rodent:\*

12: sp\_virus:\*

13: sp\_vertebrate:\*

14: sp\_unclassified:\*

15: sp\_rvirus:\*

16: sp\_bacteriap:\*

17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	798	98.3	133	4	Q96KJ8
2	792	97.5	193	6	Q9BG15
3	654	80.5	178	6	Q9MZL8
4	648	79.8	193	6	Q9GL09
5	634	78.1	192	6	Q95W33
6	633	78.0	192	6	Q95B38
7	626	77.1	192	6	Q9N1P7
8	536.5	66.1	195	11	Q80Y07
9	515	63.4	189	11	Q80SS8
10	441	54.3	196	11	Q91Z66
11	313	38.5	84	6	Q95LE7
12	204	25.1	45	4	Q9NQ49
13	193	23.8	211	13	Q98SQ1
14	184.5	22.7	198	13	Q8AV26
15	182.5	22.5	198	13	Q918D2
16	86.5	10.7	376	11	Q8K4E7

17	86.5	10.7	376	11	Q8K4E6	Q8K4E6 mus musculu
18	85	10.5	252	11	Q8JZN4	Q8JZN4 mus musculu
19	85	10.5	381	3	O43031	O43031 schizosacch
20	84.5	10.4	376	11	Q8K4E8	Q8K4E8 mus musculu
21	83.5	10.3	454	6	Q8HZU7	Q8HZU7 tonatia sau
22	83.5	10.3	454	6	Q8HZU6	Q8HZU6 tonatia sau
23	83.5	10.3	454	6	Q8HZU5	Q8HZU5 tonatia sau
24	83	10.2	376	11	Q8JZN0	Q8JZN0 mus musculu
25	82.5	10.2	288	6	Q865X7	Q865X7 lama glama
26	82	10.1	263	3	O74316	O74316 schizosacch
27	82	10.1	1534	5	Q8MPV7	Q8MPV7 caenorhabdi
28	81.5	10.0	599	5	Q8I2G6	Q8I2G6 plasmodium
29	81.5	10.0	617	5	Q25986	Q25986 plasmodium
30	81.5	10.0	1049	2	Q93KF0	Q93KF0 caldicellul
31	80.5	9.9	825	5	Q8IC17	Q8IC17 plasmodium
32	80.5	9.9	866	16	O84500	O84500 chlamydia t
33	79.5	9.8	595	10	Q9SDM4	Q9SDM4 dunaliella
34	79.5	9.8	1044	3	O94173	O94173 pneumocysti
35	79	9.7	452	16	O25249	O25249 helicobact
36	79	9.7	10578	5	Q8ISF5	Q8ISF5 caenorhabdi
37	79	9.7	18519	5	Q8ISF6	Q8ISF6 caenorhabdi
38	79	9.7	18534	5	Q8ISF7	Q8ISF7 caenorhabdi
39	78.5	9.7	204	2	Q9ZNF7	Q9ZNF7 clostridium
40	78.5	9.7	1061	16	Q8DU02	Q8DU02 streptococc
41	78	9.6	261	16	Q8CU21	Q8CU21 streptococc
42	78	9.6	277	16	Q8DU44	Q8DU44 streptococc
43	78	9.6	473	5	O16673	O16673 caenorhabdi
44	78	9.6	2578	5	Q8IJP9	Q8IJP9 plasmodium
45	77.5	9.5	454	6	Q8HZU4	Q8HZU4 tonatia bid

## ALIGNMENTS

RESULT 1

Q96KJ8 ID Q96KJ8 PRELIMINARY; PRT; 193 AA.  
AC Q96KJ8; Q80Y07  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Interleukin 18.  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Ying P., Jianxin L.;  
RT "Cloning of Mutant Human Interleukin 18 cDNA";  
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF380360; AAK57024.1; -;  
DR GO; GO:0005576; C:extracellular; IEA.  
DR GO; GO:0005149; F:interleukin-1 receptor binding; IEA.  
DR GO; GO:0006955; P:immune response; IEA.  
DR InterPro; IPR008996; Cytok\_IL1-like.  
DR InterPro; IPR000975; Interleukin\_1.  
DR SMART; SM00125; IL1; 1.  
SQ SEQUENCE 193 AA; 22323 MW; 2E500205D1B7E5F7 CRC64;

Query Match 98.3%; Score 798; DB 4; Length 193;  
Best Local Similarity 97.5%; Pred. NO. 2.7e-71;  
Matches 153; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 YFGKLSKLSVIRNLNDQVLFDQGNRPFDFTDSDCRDNAPRTIFISMYKDSQPRGM 60  
Db 37 YFGKLSKLSVIRNLNDQVLFDQGNRPFDFTDSDCRDNAPRTIFISMYKDSQPRGM 96  
QY 61 AVTISVKCKISXLSCKNIIISFKEMNPPDNKDKTSIIFFORSVPGHDKNMQFESSY 120  
Db 97 AVTISVKCKISXLSCKNIIISFKEMNPPDNKDKTSIIFFORSVPGHDKNMQFESSY 156  
QY 121 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNE 157





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SQ SEQUENCE 195 AA; 22172 MW; C6P815317953154D CRC64;

Query Match 66.1%; Score 536.5; DB 11; Length 195;
Best Local Similarity 65.8%; Pred. No. 2.5e-45;
Matches 100; Conservative 29; Mismatches 22; Indels 1; Gaps 1;

QY 2 FGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTIFIISMYKDSOPRGMA 61
DB 39 FGLRSTATTAVIRNMNDYVLFIDREKSPVFEEDMPADQKANEATRLIIYMYKTDNPGGL 98
QY 62 VTISVKCEKISXLSCKENKIISFKEMNPPDNIDKTSDIIFQORSVPGHDKNMQFESSY 121
DB 99 VTLVKDQTTMTLSCNKKIISFEEMPPENIDTSDLIFFQKRVPGH-NKMKFESSLYK 157

QY 122 GYFLACEKERDLFKLILKKEDELGDGRSIMFTVQ 153
DB 158 GHFLACQKEDDAFKLILKKEDELGDGRSVMFTV 189

RESULT 9
Q9CS88 PRELIMINARY; PRT; 189 AA.
AC Q80SS8
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Interleukin 18.
GN IL18.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B10.S/DvTe, and SuL/J; TISSUE=Spleen;
RA Gao J., Teuscher C.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY157834; AAO21309.1; -
DR EMBL; AY157835; AAO21310.1; -
DR InterPro; IPR008996; CytoK_IL1_like.
SQ SEQUENCE 189 AA; 21862 MW; E8F9E5EC01864665 CRC64;

Query Match 63.4%; Score 515; DB 11; Length 189;
Best Local Similarity 64.9%; Pred. No. 3.2e-43;
Matches 100; Conservative 27; Mismatches 25; Indels 2; Gaps 2;

QY 2 FGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTIFIISMYKDSOPRGMA 61
DB 34 FGLRHCTTAVIRNINDQVLFVDK-RQVFEDMTDIDQSASERQTRLIYMYKDSVVRGLA 92
QY 62 VTISVKCEKISXLSCKENKIISFKEMNPPDNIDKTSDIIFQORSVPGHDKNMQFESSY 121
DB 93 VTLVADSQMTSLSCNKKIISFEEMPPENIDTSDLIFFQKRVPGH-NKMKFESSLYE 151

QY 122 GYFLACEKERDLFKLILKKEDELGDGRSIMFTVQ 155
DB 152 GHFLACQKEDDAFKLILKKEDELGDGRSVMFTLTN 185

RESULT 10
Q91Z66 PRELIMINARY; PRT; 196 AA.
AC Q91Z66;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Interleukin 18.
GN IL18.
OS Sigmodon hispidus (Hispid cotton rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC Sigmodon.
OX NCBI_TaxID=42415;
```

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RN SEQUENCE FROM N.A.
RP Blanco J.C., Pletneva L.M., Prince G.A.;
RT "Sigmodon hispidus cytokines, chemokines and interferons.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY059406; AAL26703.1; -
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005149; P:interleukin-1 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR008996; CytoK_IL1_like.
DR InterPro; IPR000975; Interleukin_1.
DR SMART; SM00125; IL1; 1.
SQ SEQUENCE 196 AA; 22545 MW; E27C5BDC397F951C CRC64;

Query Match 54.3%; Score 441; DB 11; Length 196;
Best Local Similarity 59.4%; Pred. No. 7.5e-36;
Matches 92; Conservative 24; Mismatches 37; Indels 2; Gaps 2;

QY 2 FGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTIFIISMYK-DSOPRGM 60
DB 39 FFKESSTTAVIRNMNDYVLFIDREKSPVFEEDMPADQKANEATRLIIYMYKTDNPGGL 98
QY 61 AVTISVKCEKISXLSCKENKIISFKEMNPPDNIDKTSDIIFQORSVPGHDKNMQFESSY 120
DB 99 PVTLSVRDRMTLSCNKKIISFEEMDPPLDGTGKSDLIFFQRAVPGH-NKMKFESSILH 157

QY 121 EGYFLACEKERDLFKLILKKEDELGDGRSIMFTVQ 155
DB 158 EGHFLACRDRGDSFKLILKKEDELGDGRSIFITVTN 192

RESULT 11
Q95LE7 PRELIMINARY; PRT; 84 AA.
AC Q95LE7;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE IL-18 (Fragment).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA Chamizo C., Rubio J.M., Moreno J., Alvar J.;
RT "Semi-quantification of canine cytokine expression by one tube RT-PCR.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF327900; AAL26920.1; -
DR InterPro; IPR008996; CytoK_IL1_like.
FT NON_TER 1 1
FT NON_TER 84 84
SQ SEQUENCE 84 AA; 9568 MW; 19BD9E27F336774B CRC64;

Query Match 38.5%; Score 313; DB 6; Length 84;
Best Local Similarity 74.7%; Pred. No. 1.5e-23;
Matches 59; Conservative 10; Mismatches 10; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTIFIISMYKDSOPRGM 60
DB 5 YFGKLEPKLSIIRNLNDQVLFVNEGQPVFEEDMPDSDCTDNAPHTIFIYMYKDSLTRL 64
QY 61 AVTISVKCEKISXLSCKEN 79
DB 65 AVTISVKYKTMSTLSCNK 83

RESULT 12
Q9NQ49 PRELIMINARY; PRT; 45 AA.
ID Q9NQ49
AC Q9NQ49;
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DT 01-OCT-2000 (Tremblrel. 15, Created)  
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)  
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
DE Interleukin-18 (Fragment).  
GN IL-18.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Fathan A.J., Pravica V., Hutchinson I.V.;  
RL "Identification of Human Interleukin-18 gene polymorphisms";  
DR EMBL; AJ295724; CAC01436.1; -  
DR InterPro; IPR008996; Cytok\_IL1\_like.  
FT NON TER 1  
FT NON TER 45  
SQ SEQUENCE 45 AA; 5266 MW; DF3A626507E3D61A CRC64;

Query Match 25.1%; Score 204; DB 4; Length 45;  
Best Local Similarity 100.0%; Pred. No. 4.7e-13;  
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 YFGKLESLVIRNLNDQVLFIDQGNRPLFEDMTDSDCR 39  
DB 7 YFGKLESLVIRNLNDQVLFIDQGNRPLFEDMTDSDCR 45

RESULT 13  
Q98SQ1 PRELIMINARY; PRT; 211 AA.  
AC Q98SQ1:  
DT 01-JUN-2001 (Tremblrel. 17, Created)  
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)  
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
DE Interleukin-18 (Fragment).  
GN IL-18.  
OS Anas platyrhynchos (Domestic duck).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.  
OX NCBI\_TaxID=8839;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Chan W.-S., Warr G.W., Middleton D.L., Lundquist M.L., Higgins D.A.;  
RL "Anas platyrhynchos T-cell antigens, IL-18 gene";  
DR EMBL; AF336122; AAK26322.1; -  
DR GO; GO:0005576; C:extracellular; IEA.  
DR GO; GO:0005149; F:interleukin-1 receptor binding; IEA.  
DR GO; GO:0006955; P:immune response; IEA.  
DR InterPro; IPR008996; Cytok\_IL1\_like.  
DR InterPro; IPR000975; Interleukin\_1.  
DR SMART; SM00125; IL1; 1.  
FT NON TER 1  
FT NON TER 1  
SQ SEQUENCE 211 AA; 24541 MW; CA6FC63538211B2B CRC64;

Query Match 23.8%; Score 193; DB 13; Length 211;  
Best Local Similarity 36.5%; Pred. No. 3.3e-11;  
Matches 61; Conservative 29; Mismatches 63; Indels 14; Gaps 9;  
QY 2 FGKLESLVIRNLNDQVLFIDQGNRPLFEDMTDSDCRNAPRTIFIIISMYKDSQP-RG 59  
DB 43 FSKETLHFRNVNSQVLRPLDNLMAAFEDVTDQEMKSGGNV-FCHHCYKTTTSPAG 101

QY 60 MAVTISVKCE-KISLSCENK-----IISFKEMNPDPNIKDTKSDIIFQRSVPGHDK-M 113  
DB 102 MPVAFSVRVEDKSYMCEEBHGKMWVFRGEVPEKIPG-ESNLIIFPKFTTTSYSSKAF 160  
QY 114 QFESSVVEGYFLACEKRDLPKILKK---EDELGDRS-INFTVONE 156  
DB 161 KFEYSLRGRMFLAFEEEDSLRKLILKKLPREDEVDETTKILTSHNE 207

Query Match 24.5%; Score 182.5; DB 13; Length 198;  
Best Local Similarity 34.9%; Pred. No. 2.2e-10;  
Matches 58; Conservative 30; Mismatches 65; Indels 13; Gaps 7;  
QY 2 FGKLESLVIRNLNDQVLFIDQGNRPLFEDMTDSDCRNAPRTIFIIISMYKDSQP-RG 59  
DB 31 FCKEKTIKLFRNVNSQVLRPLDNLMAAFEDVTDQEMKSGS-GMYFDIHCYKTTTAPAG 89

QY 60 MAVTISVKCEKISLSCENK-----IISFKEMNPDPNIKDTKSDIIFQRSVPGHDK-M 113  
DB 90 MPVAFSVQVEDKSYMCEEBHGKMWVFRGEVPEKIPG-ESNMIFFKFTTSCSKAF 148  
QY 114 QFESSVVEGYFLACEKRDLPKILKK---EDELGDRSINFTVONE 156  
DB 149 KFEYSLRGRMFLAFEEEDSLRKLILKKLPREDEVDETTKFVTSRNE 194

RESULT 15  
Q918D2 PRELIMINARY; PRT; 198 AA.  
AC Q918D2:  
DT 01-OCT-2000 (Tremblrel. 15, Created)  
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)  
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
DE Interleukin 18.  
GN Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20508574; PubMed=11054275;  
RA Schneider K., Puehler F., Baeuerle D., Elvers S., Staeheli P.,  
RA Kaspers B., Weining K.C.;  
RL "cDNA cloning of biologically active chicken Interleukin-18";  
DR J. Interferon Cytokine Res. 20:879-883(2000).  
DR EMBL; AJ277865; CAB96214.1; -  
DR InterPro; IPR008996; Cytok\_IL1\_like.  
FT CHAIN 30 198 INTERLEUKIN 18.  
SQ SEQUENCE 198 AA; 22918 MW; 29BB77DC3E3C6600 CRC64;

Query Match 22.7%; Score 184.5; DB 13; Length 198;  
Best Local Similarity 34.9%; Pred. No. 2.2e-10;  
Matches 58; Conservative 30; Mismatches 65; Indels 13; Gaps 7;  
QY 2 FGKLESLVIRNLNDQVLFIDQGNRPLFEDMTDSDCRNAPRTIFIIISMYKDSQP-RG 59  
DB 31 FCKEKTIKLFRNVNSQVLRPLDNLMAAFEDVTDQEMKSGS-GMYFDIHCYKTTTAPAG 89

RESULT 14  
Q8AV26 PRELIMINARY; PRT; 198 AA.  
AC Q8AV26:  
DT 01-MAR-2003 (Tremblrel. 23, Created)  
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)  
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
DE Interleukin-18 precursor (Fragment).  
GN IL-18.  
OS Meleagris gallopavo (Common turkey).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Meleagris.  
OX NCBI\_TaxID=9103;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22195503; PubMed=12206831;  
RA Kaiser P.;  
RL "Turkey and chicken interleukin-18 (IL18) share high sequence identity, but have different polyadenylation sites in their 3' UTR";  
DR Dev. Comp. Immunol. 26:681-687(2002).  
DR EMBL; AJ312000; CAC83483.1; -  
DR InterPro; IPR008996; Cytok\_IL1\_like.  
KW Signal.  
FT NON TER 1  
FT SIGNAL <1 28 POTENTIAL.  
FT CHAIN 29 198 INTERLEUKIN-18.  
SQ SEQUENCE 198 AA; 22967 MW; AID450BC7207BFAD CRC64;

Query Match 22.7%; Score 184.5; DB 13; Length 198;  
Best Local Similarity 34.9%; Pred. No. 2.2e-10;  
Matches 58; Conservative 30; Mismatches 65; Indels 13; Gaps 7;  
QY 2 FGKLESLVIRNLNDQVLFIDQGNRPLFEDMTDSDCRNAPRTIFIIISMYKDSQP-RG 59  
DB 31 FCKEKTIKLFRNVNSQVLRPLDNLMAAFEDVTDQEMKSGS-GMYFDIHCYKTTTAPAG 89

QY 60 MAVTISVKCEKISLSCENK-----IISFKEMNPDPNIKDTKSDIIFQRSVPGHDK-M 113  
DB 90 MPVAFSVQVEDKSYMCEEBHGKMWVFRGEVPEKIPG-ESNMIFFKFTTSCSKAF 148  
QY 114 QFESSVVEGYFLACEKRDLPKILKK---EDELGDRSINFTVONE 156  
DB 149 KFEYSLRGRMFLAFEEEDSLRKLILKKLPREDEVDETTKFVTSRNE 194

RESULT 15  
Q918D2 PRELIMINARY; PRT; 198 AA.  
AC Q918D2:  
DT 01-OCT-2000 (Tremblrel. 15, Created)  
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)  
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
DE Interleukin 18.  
GN Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20508574; PubMed=11054275;  
RA Schneider K., Puehler F., Baeuerle D., Elvers S., Staeheli P.,  
RA Kaspers B., Weining K.C.;  
RL "cDNA cloning of biologically active chicken Interleukin-18";  
DR J. Interferon Cytokine Res. 20:879-883(2000).  
DR EMBL; AJ277865; CAB96214.1; -  
DR InterPro; IPR008996; Cytok\_IL1\_like.  
FT CHAIN 30 198 INTERLEUKIN 18.  
SQ SEQUENCE 198 AA; 22918 MW; 29BB77DC3E3C6600 CRC64;

Query Match 22.5%; Score 182.5; DB 13; Length 198;  
Best Local Similarity 34.9%; Pred. No. 2.2e-10;  
Matches 58; Conservative 30; Mismatches 65; Indels 13; Gaps 7;  
QY 2 FGKLESLVIRNLNDQVLFIDQGNRPLFEDMTDSDCRNAPRTIFIIISMYKDSQP-RG 59  
DB 31 FCKEKTIKLFRNVNSQVLRPLDNLMAAFEDVTDQEMKSGS-GMYFDIHCYKTTTAPAG 89

QY 60 MAVTISVKCEKISLSCENK-----IISFKEMNPDPNIKDTKSDIIFQRSVPGHDK-M 113  
DB 90 MPVAFSVQVEDKSYMCEEBHGKMWVFRGEVPEKIPG-ESNMIFFKFTTSCSKAF 148  
QY 114 QFESSVVEGYFLACEKRDLPKILKK---EDELGDRSINFTVONE 156  
DB 149 KFEYSLRGRMFLAFEEEDSLRKLILKKLPREDEVDETTKFVTSRNE 194

RESULT 15  
Q918D2 PRELIMINARY; PRT; 198 AA.  
AC Q918D2:  
DT 01-OCT-2000 (Tremblrel. 15, Created)  
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)  
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
DE Interleukin 18.  
GN Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20508574; PubMed=11054275;  
RA Schneider K., Puehler F., Baeuerle D., Elvers S., Staeheli P.,  
RA Kaspers B., Weining K.C.;  
RL "cDNA cloning of biologically active chicken Interleukin-18";  
DR J. Interferon Cytokine Res. 20:879-883(2000).  
DR EMBL; AJ277865; CAB96214.1; -  
DR InterPro; IPR008996; Cytok\_IL1\_like.  
FT CHAIN 30 198 INTERLEUKIN 18.  
SQ SEQUENCE 198 AA; 22918 MW; 29BB77DC3E3C6600 CRC64;

Query Match 22.5%; Score 182.5; DB 13; Length 198;  
Best Local Similarity 34.9%; Pred. No. 2.2e-10;  
Matches 58; Conservative 30; Mismatches 65; Indels 13; Gaps 7;  
QY 2 FGKLESLVIRNLNDQVLFIDQGNRPLFEDMTDSDCRNAPRTIFIIISMYKDSQP-RG 59  
DB 31 FCKEKTIKLFRNVNSQVLRPLDNLMAAFEDVTDQEMKSGS-GMYFDIHCYKTTTAPAG 89

QY 60 MAVTISVKCEKISLSCENK-----IISFKEMNPDPNIKDTKSDIIFQRSVPGHDK-M 113  
DB 90 MPVAFSVQVEDKSYMCEEBHGKMWVFRGEVPEKIPG-ESNMIFFKFTTSCSKAF 148  
QY 114 QFESSVVEGYFLACEKRDLPKILKK---EDELGDRSINFTVONE 156  
DB 149 KFEYSLRGRMFLAFEEEDSLRKLILKKLPREDEVDETTKFVTSRNE 194





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OM protein - protein search, using sw model

Run on: August 19, 2004, 13:34:05 ; Search time 19 Seconds  
(without alignments)  
426.594 Million cell updates/sec

Title: US-09-716-356A-6  
Perfect score: 812  
Sequence: 1 YFGKLESKLSVIRNLNDQVL.....LKKDELGDRLSMTFVQNE 157

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/2/iaa/5A COMB.pep.\*  
2: /cgn2\_6/ptodata/2/iaa/5B COMB.pep.\*  
3: /cgn2\_6/ptodata/2/iaa/6A COMB.pep.\*  
4: /cgn2\_6/ptodata/2/iaa/6B COMB.pep.\*  
5: /cgn2\_6/ptodata/2/iaa/PCTUS COMB.pep.\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	811	99.9	157	4	US-08-982-285-4
2	811	99.9	157	4	US-09-700-609-1
3	811	99.9	157	4	US-09-398-412B-7
4	810	99.8	157	2	US-08-896-605A-6
5	810	99.8	157	2	US-08-896-501A-4
6	810	99.8	157	3	US-08-884-324-1
7	810	99.8	157	3	US-08-996-338-26
8	810	99.8	157	3	US-08-558-818-1
9	810	99.8	157	3	US-08-974-469A-1
10	810	99.8	157	3	US-08-832-180-1
11	810	99.8	157	3	US-08-832-198-6
12	810	99.8	157	4	US-09-819-902-6
13	810	99.8	157	4	US-09-752-510-6
14	810	99.8	157	4	US-09-711-899-1
15	810	99.8	157	4	US-09-556-972-26
16	810	99.8	157	4	US-09-649-063-1
17	810	99.8	157	4	US-08-896-605A-2
18	810	99.8	157	2	US-08-896-501A-2
19	810	99.8	157	3	US-08-832-180-9
20	801	99.6	157	4	US-08-982-285-6
21	792	97.5	157	4	US-09-597-576-2
22	791	97.4	157	4	US-08-982-285-7
23	791	97.4	157	4	US-08-982-285-8
24	782	96.3	157	4	US-08-982-285-11
25	781	96.2	157	4	US-08-982-285-9
26	772	95.1	157	4	US-08-982-285-12
27	771	95.0	157	4	US-08-982-285-10

28	613	75.5	179	4	US-09-445-724B-14	Sequence 14, Appl
29	613	75.5	133	4	US-09-445-724B-2	Sequence 2, Appl
30	613	75.5	193	4	US-09-445-724B-6	Sequence 6, Appl
31	517	63.7	157	4	US-08-982-285-13	Sequence 13, Appl
32	515	63.4	157	4	US-08-982-285-5	Sequence 5, Appl
33	515	63.4	157	4	US-09-700-609-2	Sequence 2, Appl
34	515	63.4	158	4	US-09-398-412B-8	Sequence 8, Appl
35	513	63.2	157	2	US-08-502-535B-2	Sequence 2, Appl
36	513	63.2	157	2	US-08-908-005A-2	Sequence 2, Appl
37	513	63.2	157	3	US-08-996-338-27	Sequence 7, Appl
38	513	63.2	157	3	US-08-558-818-7	Sequence 7, Appl
39	513	63.2	157	3	US-08-974-469A-7	Sequence 7, Appl
40	513	63.2	157	3	US-08-832-180-8	Sequence 8, Appl
41	513	63.2	157	3	US-08-832-198-11	Sequence 11, Appl
42	513	63.2	157	3	US-09-253-523-2	Sequence 2, Appl
43	513	63.2	157	3	US-09-251-911-2	Sequence 2, Appl
44	513	63.2	157	4	US-09-819-902-11	Sequence 11, Appl
45	513	63.2	157	4	US-09-752-510-11	Sequence 11, Appl

## ALIGNMENTS

RESULT 1  
US-08-982-285-4  
; Sequence 4, Application US/08982285  
; Patent No. 6476197  
; GENERAL INFORMATION:  
; APPLICANT: YAMAMOTO, Koza  
; APPLICANT: OKAMOTO, Iwao  
; APPLICANT: KURIMOTO, Masashi  
; TITLE OF INVENTION: POLYPEPTIDES  
; NUMBER OF SEQUENCES: 51  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.  
; STREET: 419 7th Street N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/982,285  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 333,037/96  
; FILING DATE: No. 6476197ember 29, 1996  
; APPLICATION NUMBER: JP 20,906/97  
; FILING DATE: January 21, 1997  
; APPLICATION NUMBER: JP 10,053,503  
; FILING DATE: No. 6476197ember 14, 1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BROWDY, Roger L.  
; REGISTRATION NUMBER: 25,618  
; REFERENCE/DOCKET NUMBER: YAMAMOTO=15  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 157 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-982-285-4

Query Match 99.9%; Score 811; DB 4; Length 157;  
Best Local Similarity 99.4%; Pred. No. 3.8e-88;  
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Query_Match . 99.9%; Score 811; DB 4; Length 158;
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	Best Local Similarity	100.0%	Pred. No. 4.9e-08		
	Matches 157	Conservative 0	Mismatches 0	Indels 0	Gaps 0
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Db	1	YFGKLEKLSVIRNLNDQVLFI	DQGNRPLFEDMTDSCRDNAPRTIF	IIISMVKDSQPRGM	60
Qy	61	AVTISVCKEISLXSCENKII	SFKEMPPDNI	KTKSDII	IFFQSRVPGHDKMVFESSY 120
Db	61	AVTISVCKEISLXSCENKII	SFKEMPPDNI	KTKSDII	IFFQSRVPGHDKMVFESSY 120

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QY 121 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNEED 157
Db 121 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNEED 157

RESULT 5
US-08-896-501A-4
; Sequence 4, Application US/08896501A
; Patent No. 5891663
; GENERAL INFORMATION:
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PROCESS FOR PRODUCING POLYPEPTIDE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/896,501A
; FILING DATE: 18-JUL-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 213,267/1996
; FILING DATE: 25-JUL-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 31,474/1997
; FILING DATE: 31-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: TANIMOTO=3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-896-501A-4

Query Match 99.8%; Score 810; DB 2; Length 157;
Best Local Similarity 100.0%; Pred. No. 4.9e-88;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60

QY 61 AVTISVKCEKISXLSNCKIISFKEMNPPDNIKDTKSDIIFQFORSVPGHDKMKQFESSY 120
Db 61 AVTISVKCEKISXLSNCKIISFKEMNPPDNIKDTKSDIIFQFORSVPGHDKMKQFESSY 120

QY 121 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNEED 157
Db 121 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNEED 157

RESULT 6
US-08-884-324-1
; Sequence 1, Application US/08884324
; Patent No. 6060283
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; GENERAL INFORMATION:
; APPLICANT: Takanori OKURA
; APPLICANT: Kakuji TORIGOE
; APPLICANT: Masashi KURIMOTO
; TITLE OF INVENTION: GENOMIC DNA ENCODING A POLYPEPTIDE CAPABLE
; OF INDUCING THE PRODUCTION OF INTERFERON-
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/884,324
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 185,305/96
; FILING DATE: 27-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: OKURA=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-884-324-1

Query Match 99.8%; Score 810; DB 3; Length 157;
Best Local Similarity 100.0%; Pred. No. 4.9e-88;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60

QY 61 AVTISVKCEKISXLSNCKIISFKEMNPPDNIKDTKSDIIFQFORSVPGHDKMKQFESSY 120
Db 61 AVTISVKCEKISXLSNCKIISFKEMNPPDNIKDTKSDIIFQFORSVPGHDKMKQFESSY 120

QY 121 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNEED 157
Db 121 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNEED 157

RESULT 7
US-08-996-338-26
; Sequence 26, Application US/08996338
; Patent No. 6087116
; GENERAL INFORMATION:
; APPLICANT: TORIGOE, Kakuji
; APPLICANT: OKURA, Takanori
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: POLYPEPTIDES
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
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;; COUNTRY: USA  
;; ZIP: 20004  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patent In Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/996,338  
;; FILING DATE: 22-DEC-1997  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: JP 74,697/1997  
;; FILING DATE: 12-MAR-1997  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: JP 215,488/1997  
;; FILING DATE: 28-JUL-1997  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: JP 291,837/1997  
;; FILING DATE: 09-OCT-1997  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: BROWDY, Roger L.  
;; REGISTRATION NUMBER: 25,618  
;; REFERENCE/DOCKET NUMBER: TORIGOE=3  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 202-628-5197  
;; TELEFAX: 202-737-3528  
;; INFORMATION FOR SEQ ID NO: 26:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 157  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
US-08-996-338-26

Query Match 99.8%; Score 810; DB 3; Length 157;  
Best Local Similarity 100.0%; Pred. No. 4.9e-88;  
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60  
QY 61 AVTISVKCEKISXLSCEKNKIISFKEMNPPDNIKDTSDIIFQRSVPGHDNKMQFESSY 120  
DB 61 AVTISVKCEKISXLSCEKNKIISFKEMNPPDNIKDTSDIIFQRSVPGHDNKMQFESSY 120  
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157  
DB 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 8  
US-08-558-818-1  
; Sequence 1, Application US/08558818  
; Patent No. 6197297  
; GENERAL INFORMATION:  
; APPLICANT: NAME: KABUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU  
; APPLICANT: KENKYUJO  
; APPLICANT: KUNIKATA, Toshio  
; APPLICANT: TANIGUCHI, Mutsuko  
; APPLICANT: KOHNO, Keizo  
; APPLICANT: KURIMOTO, Masashi  
; TITLE OF INVENTION: MONOCLONAL ANTIBODY SPECIFIC TO POLYPEPTIDE  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Browdy and Neimark  
; STREET: 419 Seventh Street N.W. Ste. 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004

;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Word Perfect Version 5.0  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Browdy, Roger L.  
;; REGISTRATION NUMBER: 25,618  
;; REFERENCE/DOCKET NUMBER: FELICI=1  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (202) 628-5197  
;; TELEFAX: (202) 737-3528  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/558,818  
;; FILING DATE:  
;; CLASSIFICATION: 530  
;; PRIOR APPLICATION DATA:  
;; PRIOR APPLICATION DATA: JP 58,240/95  
;; PRIOR APPLICATION DATA: February 23, 1995  
;; INFORMATION FOR SEQ ID NO: 1:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 157 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
US-08-558-818-1  
Query Match 99.8%; Score 810; DB 3; Length 157;  
Best Local Similarity 100.0%; Pred. No. 4.9e-88;  
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60  
DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60  
QY 61 AVTISVKCEKISXLSCEKNKIISFKEMNPPDNIKDTSDIIFQRSVPGHDNKMQFESSY 120  
DB 61 AVTISVKCEKISXLSCEKNKIISFKEMNPPDNIKDTSDIIFQRSVPGHDNKMQFESSY 120  
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157  
DB 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157  
RESULT 9  
US-08-974-469A-1  
; Sequence 1, Application US/08974469A  
; Patent No. 6207641  
; GENERAL INFORMATION:  
; APPLICANT: KABUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU  
; APPLICANT: KENKYUJO  
; APPLICANT: TORIGOE, Kakuji  
; APPLICANT: TANIMOTO, Tadao  
; APPLICANT: FUKUDA, Shigeharu  
; APPLICANT: KURIMOTO, Masashi  
; TITLE OF INVENTION: AGENT FOR SUSCEPTIVE DISEASE  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Browdy and Neimark  
; STREET: 419 Seventh Street N.W. Ste. 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Word Perfect Version 5.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/974,469A  
; FILING DATE:  
; CLASSIFICATION:

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/599,879
; FILING DATE: March 10, 1995
; APPLICATION NUMBER: JP 78,357/95
; FILING DATE: March 10, 1995
; APPLICATION NUMBER: JP 274,988/95
; FILING DATE: September 29, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Browdy, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: TORIGOE=1A
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-974-469A-1

Query Match 99.8%; Score 810; DB 3; Length 157;
Best Local Similarity 100.0%; Pred. No. 4.9e-88;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDRNAPRTTIFIISMVKDSQPRGM 60
|
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDRNAPRTTIFIISMVKDSQPRGM 60
|
QY 61 AVTISVKCEKISXLSKCNKIISFKENPPDNIKDTKSDIIFQORSVPGHDKMKQFESSY 120
|
Db 61 AVTISVKCEKISXLSKCNKIISFKENPPDNIKDTKSDIIFQORSVPGHDKMKQFESSY 120
|
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
|
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
|

RESULT 10
US-08-832-180-1
; Sequence 1, Application US/08832180
; Patent No. 6214584
; GENERAL INFORMATION:
; APPLICANT: KASUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU
; APPLICANT: KENYUJO
; APPLICANT: USHIO, Shimpel
; APPLICANT: TORIGOE, Kakuji
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: OKAMURA, Haruki
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: INTERFERON- PRODUCTION INDUCING
; TITLE OF INVENTION: POLYPEPTIDE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street N.W. Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect Version 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/832,180
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/559,191
; FILING DATE:

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/599,879
; FILING DATE: March 10, 1995
; APPLICATION NUMBER: JP 78,357/95
; FILING DATE: March 10, 1995
; APPLICATION NUMBER: JP 274,988/95
; FILING DATE: September 29, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Browdy, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: TORIGOE=1A
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-974-469A-1

Query Match 99.8%; Score 810; DB 3; Length 157;
Best Local Similarity 100.0%; Pred. No. 4.9e-88;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDRNAPRTTIFIISMVKDSQPRGM 60
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Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDRNAPRTTIFIISMVKDSQPRGM 60
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QY 61 AVTISVKCEKISXLSKCNKIISFKENPPDNIKDTKSDIIFQORSVPGHDKMKQFESSY 120
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Db 61 AVTISVKCEKISXLSKCNKIISFKENPPDNIKDTKSDIIFQORSVPGHDKMKQFESSY 120
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QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
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Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
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RESULT 11
US-08-832-198-6
; Sequence 6, Application US/08832198
; Patent No. 6242255
; GENERAL INFORMATION:
; APPLICANT: AKITA, Kenji
; APPLICANT: NUKADA, Yoshiyuki
; APPLICANT: FUJII, Mitsukiyo
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PROTEIN WHICH INDUCES INTERLEUKIN-GAMMA
; TITLE OF INVENTION: PRODUCTION BY IMMUNOCOMPETENT CELL
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/832,198
; FILING DATE: 08-APR-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/721,018
; FILING DATE: 25-SEP-1996
; APPLICATION NUMBER: JP 95-270725
; FILING DATE: 26-SEP-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 96-067434
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;
; FILING DATE: 29-FEB-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP not yet received
; FILING DATE: 20-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: AKITA-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; OTHER INFORMATION: "Xaa" in position 73 is either
; OTHER INFORMATION: 'ile' or 'thr'
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US-08-832-198-6

Query Match          99.8%; Score 810; DB 3; Length 157;
Best Local Similarity 100.0%; Pred. No. 4.9e-88;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 60
Qy 61 AVTISVCKEKLXSLSCENKLIISFKEMNPPDNIKTKSDIIFQSVPGHDNKMQFESSY 120
Db 61 AVTISVCKEKLXSLSCENKLIISFKEMNPPDNIKTKSDIIFQSVPGHDNKMQFESSY 120
Qy 121 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNE 157
Db 121 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNE 157

RESULT 12
US-09-819-902-6
; Sequence 6, Application US/09819902
; Patent No. 6403079
; GENERAL INFORMATION:
; APPLICANT: AKITA, Kenji
; NUKADA, Yoshiyuki
; FUJII, Mitsuakiyo
; TANIMOTO, Tadao
; KURIMOTO, Masashi
;
; TITLE OF INVENTION: PROTEIN WHICH INDUCES INTERLEUKIN-GAMMA
;
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/819,902
; FILING DATE: 29-Mar-2001
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/832,798
; FILING DATE: 25-SEP-1996
; APPLICATION NUMBER: JP 95-270725
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; FILING DATE: 26-SEP-1995
; APPLICATION NUMBER: JP 96-067434
; FILING DATE: 29-FEB-1996
; APPLICATION NUMBER: JP not yet received
; FILING DATE: 20-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: AKITA-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; OTHER INFORMATION: "Xaa" in position 73 is either
; OTHER INFORMATION: 'ile' or 'thr'
;
US-09-819-902-6

Query Match          99.8%; Score 810; DB 4; Length 157;
Best Local Similarity 100.0%; Pred. No. 4.9e-88;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 60
Qy 61 AVTISVCKEKLXSLSCENKLIISFKEMNPPDNIKTKSDIIFQSVPGHDNKMQFESSY 120
Db 61 AVTISVCKEKLXSLSCENKLIISFKEMNPPDNIKTKSDIIFQSVPGHDNKMQFESSY 120
Qy 121 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNE 157
Db 121 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNE 157

RESULT 13
US-09-752-510-6
; Sequence 6, Application US/09752510
; Patent No. 6441138
; GENERAL INFORMATION:
; APPLICANT: AKITA, Kenji
; NUKADA, Yoshiyuki
; FUJII, Mitsuakiyo
; TANIMOTO, Tadao
; KURIMOTO, Masashi
;
; TITLE OF INVENTION: PROTEIN WHICH INDUCES INTERLEUKIN-GAMMA
;
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/752,510
; FILING DATE: 03-Jan-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/721,018
; FILING DATE: <Unknown>
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APPLICATION NUMBER: JP 96-067434  
FILING DATE: 29-FEB-1996  
APPLICATION NUMBER: JP not yet received  
FILING DATE: 20-SEP-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: BROWDY, Roger L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: AKITA-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 628-5197  
TELEFAX: (202) 737-3528  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 157 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
OTHER INFORMATION: "Xaa" in position 73 is either  
'ile' or 'Thr'  
SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
US-09-752-510-6

Query Match 99.8%; Score 810; DB 4; Length 157;  
Best Local Similarity 100.0%; Pred. No. 4.9e-88;  
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFPEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60  
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFPEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60

QY 61 AVTISVCKEKISXLSKCNKIISFKEMNPPDNIKDTSDIFFQRSVFGHDNKMQFESSY 120  
Db 61 AVTISVCKEKISXLSKCNKIISFKEMNPPDNIKDTSDIFFQRSVFGHDNKMQFESSY 120

QY 121 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNE 157  
Db 121 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNE 157

RESULT 14  
US-09-711-899-1  
Sequence 1, Application US/09711899  
Patent No. 6509449  
GENERAL INFORMATION:  
APPLICANT: <Unknown>  
TITLE OF INVENTION: MONOCLONAL ANTIBODY SPECIFIC TO POLYPEPTIDE  
WHICH INDUCES INTERFERON- PRODUCTION  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Browdy and Neimark  
STREET: 419 Seventh Street N.W. Ste. 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Word Perfect Version 5.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/711,899  
FILING DATE: 13-No. 6509449-2000  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/588,818  
FILING DATE: 2000-11-15  
ATTORNEY/AGENT INFORMATION:  
NAME: Browdy, Roger L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: FELICI=1

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 628-5197  
TELEFAX: (202) 737-3528  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 157 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-711-899-1

Query Match 99.8%; Score 810; DB 4; Length 157;  
Best Local Similarity 100.0%; Pred. No. 4.9e-88;  
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFPEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60  
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QY 61 AVTISVCKEKISXLSKCNKIISFKEMNPPDNIKDTSDIFFQRSVFGHDNKMQFESSY 120  
Db 61 AVTISVCKEKISXLSKCNKIISFKEMNPPDNIKDTSDIFFQRSVFGHDNKMQFESSY 120

QY 121 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNE 157  
Db 121 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNE 157

RESULT 15  
US-09-556-972-26  
Sequence 26, Application US/09556972  
Patent No. 6559298  
GENERAL INFORMATION:  
APPLICANT: TORIGOE, Kakuji  
OKURA, Takanori  
KURIMOTO, Masashi  
TITLE OF INVENTION: POLYPEPTIDES  
NUMBER OF SEQUENCES: 37  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/556,972  
FILING DATE: 24-Apr-2000  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/996,338  
FILING DATE: 22-DEC-1997  
APPLICATION NUMBER: JP 74,697/1997  
FILING DATE: 12-MAR-1997  
APPLICATION NUMBER: JP 215,488/1997  
FILING DATE: 28-JUL-1997  
APPLICATION NUMBER: JP 291,837/1997  
FILING DATE: 09-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: BROWDY, Roger L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: TORIGOE=3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 157

; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 26:  
US-09-556-972-26

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QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTKSDIIFQSVPGHDNKMQFESSY 120  
DB 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTKSDIIFQSVPGHDNKMQFESSY 120  
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157  
DB 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

Search completed: August 19, 2004, 13:37:15  
Job time : 20 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 19, 2004, 13:35:10 ; Search time 46 Seconds  
(without alignments)  
1072.566 Million cell updates/sec

Title: US-09-716-356A-6

Perfect score: 812

Sequence: 1 YFGKLESKLSVIRNLNDQVL.....LKKEDELGDRSIMFTVQNE 157

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1295152 seqs, 314255058 residues

Total number of hits satisfying chosen parameters: 1295152

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

- Published Applications AA:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	811	99.9	157	12	US-10-247-703-71
5	811	99.9	157	13	US-10-100-057-6
6	811	99.9	157	13	US-10-094-153-2
7	811	99.9	157	14	US-10-260-576-4
8	811	99.9	157	14	US-10-297-136-1
9	811	99.9	157	14	US-10-311-491-3
10	811	99.9	157	15	US-10-397-786A-3
11	811	99.9	157	16	US-10-280-609-1
12	811	99.9	157	16	US-10-646-308-14
13	811	99.9	158	12	US-10-695-195-7
14	811	99.9	158	16	US-10-694-978-7
15	811	99.9	177	12	US-10-247-703-69

16	811	99.9	193	9	US-09-798-075-1	Sequence 1, Appli
17	811	99.9	193	9	US-09-770-528-8	Sequence 8, Appli
18	811	99.9	193	14	US-10-311-491-1	Sequence 1, Appli
19	811	99.9	193	16	US-10-679-201-5	Sequence 5, Appli
20	811	99.9	233	14	US-10-311-491-10	Sequence 10, Appli
21	810	99.8	157	8	US-08-996-140-1	Sequence 1, Appli
22	810	99.8	157	9	US-09-924-099-21	Sequence 21, Appli
23	810	99.8	157	14	US-10-327-069-1	Sequence 1, Appli
24	810	99.8	157	14	US-10-349-023-26	Sequence 26, Appli
25	810	99.8	193	16	US-10-646-308-13	Sequence 13, Appli
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27	807	99.4	193	13	US-10-094-153-9	Sequence 9, Appli
28	805	99.1	157	13	US-10-094-153-6	Sequence 6, Appli
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31	805	99.1	193	13	US-10-094-153-4	Sequence 4, Appli
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33	803	98.9	193	14	US-10-105-080-4	Sequence 4, Appli
34	801	98.6	157	10	US-09-030-061-20	Sequence 4, Appli
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36	801	98.6	157	14	US-10-260-576-6	Sequence 6, Appli
37	799	98.4	157	12	US-10-247-703-77	Sequence 77, Appli
38	799	98.4	157	13	US-10-094-153-8	Sequence 8, Appli
39	799	98.4	193	13	US-10-094-153-5	Sequence 5, Appli
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41	795.5	98.0	156	15	US-10-414-774-1	Sequence 1, Appli
42	795	97.9	157	12	US-10-247-703-74	Sequence 74, Appli
43	792	97.5	157	12	US-10-247-703-75	Sequence 75, Appli
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45	791	97.4	157	10	US-09-030-061-22	Sequence 22, Appli

ALIGNMENTS

RESULT 1

US-09-775-046-9  
; Sequence 9, Application US/09775046  
; Patent No. US20020102234A1  
; GENERAL INFORMATION:  
; APPLICANT: Debets, Johannes Eduard Maria Antonius  
; APPLICANT: Timans, Jacqueline C.  
; APPLICANT: Bazan, J. Fernando  
; APPLICANT: Kastelein, Robert A.  
; TITLE OF INVENTION: MAMMALIAN CYTOKINES; RECEPTORS; RELATED REAGENTS AND METHODS  
; FILE REFERENCE: DX01073K  
; CURRENT APPLICATION NUMBER: US/09/775,046  
; CURRENT FILING DATE: 2001-02-01  
; PRIOR APPLICATION NUMBER: 60/179,638  
; PRIOR FILING DATE: 2000-02-02  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 9  
; LENGTH: 157  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-775-046-9

Query Match	99.9%	Score 811;	DB 9;	Length 157;
Best Local Similarity	99.4%	Pred. No. 3.1e-81;		
Matches 156;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
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Db	1	YFGKLESKLSVIRNLNDQVLFDIQGNRPLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM	60	
QY	61	AVTISVKCKIKSLSCENKIIISFKENMPDNIKDTKSDIIFQORSVPGHNDKNQMFESSY	120	
Db	61	AVTISVKCKIKSLSCENKIIISFKENMPDNIKDTKSDIIFQORSVPGHNDKNQMFESSY	120	
QY	121	EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNE 157		
Db	121	EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNE 157		

US-09-030-061-6  
; Sequence 6, Application US/09030061  
; Publication No. US20030095946A1  
; GENERAL INFORMATION:  
; APPLICANT: GILLISPIE, Matthew Todd  
; APPLICANT: HORMWOOD, Nicole Joy  
; APPLICANT: UDAGAWA, No. US20030095946A1uyuki  
; APPLICANT: KURIMOTO, Masashi  
; TITLE OF INVENTION: OSTEOCLASTGENIC INHIBITORY AGENT  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/030,061  
; FILING DATE: 25-FEB-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 55,468/1997  
; FILING DATE: 25-FEB-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BROWDY, Roger L.  
; REGISTRATION NUMBER: 25,618  
; REFERENCE/DOCKET NUMBER: GILLISPIE-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 628-5197  
; TELEFAX: (202) 737-3528  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 157 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-09-030-061-6

Query Match 99.9%; Score 811; DB 10; Length 157;  
Best Local Similarity 99.4%; Pred. No. 3.1e-81;  
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDNAPRTIFIISMYKDSQPRGM 60  
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDNAPRTIFIISMYKDSQPRGM 60  
QY 61 AVTISVKCEKISXLSKENKIIISFKEMNPPDNIKOTKSDIIFQRSVPGHDKMKQFESSY 120  
Db 61 AVTISVKCEKISXLSKENKIIISFKEMNPPDNIKOTKSDIIFQRSVPGHDKMKQFESSY 120  
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157  
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157

RESULT 3  
US-10-247-703-65  
; Sequence 65, Application US/10247703  
; Publication No. US20030063597A1  
; GENERAL INFORMATION:  
; APPLICANT: Branigan, Patrick  
; APPLICANT: Goletz, Theresa J  
; APPLICANT: Knight, David M  
; APPLICANT: McCarthy, Stephen G  
; APPLICANT: Scallion, Bernard J

; APPLICANT: Snyder, Linda A  
; TITLE OF INVENTION: NUCLEIC ACID VACCINES USING TUMOR ANTIGEN ENCODING NUCLEIC ACIDS  
; FILE REFERENCE: CEN310  
; CURRENT APPLICATION NUMBER: US/10/247,703  
; CURRENT FILING DATE: 2002-09-20  
; PRIOR APPLICATION NUMBER: 60/328,371  
; PRIOR FILING DATE: 2001-10-10  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 65  
; LENGTH: 157  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-247-703-65

Query Match 99.9%; Score 811; DB 12; Length 157;  
Best Local Similarity 99.4%; Pred. No. 3.1e-81;  
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDNAPRTIFIISMYKDSQPRGM 60  
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDNAPRTIFIISMYKDSQPRGM 60  
QY 61 AVTISVKCEKISXLSKENKIIISFKEMNPPDNIKOTKSDIIFQRSVPGHDKMKQFESSY 120  
Db 61 AVTISVKCEKISXLSKENKIIISFKEMNPPDNIKOTKSDIIFQRSVPGHDKMKQFESSY 120  
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157  
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157

## RESULT 4

US-10-247-703-71  
; Sequence 71, Application US/10247703  
; Publication No. US20030063597A1  
; GENERAL INFORMATION:  
; APPLICANT: Branigan, Patrick  
; APPLICANT: Goletz, Theresa J  
; APPLICANT: Knight, David M  
; APPLICANT: McCarthy, Stephen G  
; APPLICANT: Scallion, Bernard J  
; APPLICANT: Snyder, Linda A  
; TITLE OF INVENTION: NUCLEIC ACID VACCINES USING TUMOR ANTIGEN ENCODING NUCLEIC ACIDS  
; FILE REFERENCE: CEN310  
; CURRENT APPLICATION NUMBER: US/10/247,703  
; CURRENT FILING DATE: 2002-09-20  
; PRIOR APPLICATION NUMBER: 60/328,371  
; PRIOR FILING DATE: 2001-10-10  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 71  
; LENGTH: 157  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-247-703-71

Query Match 99.9%; Score 811; DB 12; Length 157;  
Best Local Similarity 99.4%; Pred. No. 3.1e-81;  
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDNAPRTIFIISMYKDSQPRGM 60  
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDNAPRTIFIISMYKDSQPRGM 60  
QY 61 AVTISVKCEKISXLSKENKIIISFKEMNPPDNIKOTKSDIIFQRSVPGHDKMKQFESSY 120  
Db 61 AVTISVKCEKISXLSKENKIIISFKEMNPPDNIKOTKSDIIFQRSVPGHDKMKQFESSY 120  
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157  
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157

Db 121 EGYFLACEKERDLFKLILKKEDELGDRSINFTVQNE 157

RESULT 5

US-10-100-057-6

Query Match 99.9%; Score 811; DB 13; Length 157;

Best Local Similarity 99.4%; Pred. No. 3.1e-81;

Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

APPLICANT: Kim, Soo Hyun

TITLE OF INVENTION: Interleukin-18 Mutants, Their Production and use

FILE REFERENCE: 475

CURRENT APPLICATION NUMBER: US/10/094,153

CURRENT FILING DATE: 2002-03-08

PRIOR APPLICATION NUMBER: 60/274,327

PRIOR FILING DATE: 2001-03-08

NUMBER OF SEQ ID NOS: 18

SOFTWARE: Patent in version 3.1

SEQ ID NO 2

LENGTH: 157

TYPE: PRT

ORGANISM: Homo sapiens

US-10-094-153-2

Query Match 99.9%; Score 811; DB 13; Length 157;

Best Local Similarity 99.4%; Pred. No. 3.1e-81;

Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFILSMYKDSQPRGM 60

Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFILSMYKDSQPRGM 60

Qy 61 AVTISVKCEKISLSCENKIISEKMNPPDNKDKTSIIFFQRSVPGHNDKMQFESSY 120

Db 61 AVTISVKCEKISLSCENKIISEKMNPPDNKDKTSIIFFQRSVPGHNDKMQFESSY 120

Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSINFTVQNE 157

Db 121 EGYFLACEKERDLFKLILKKEDELGDRSINFTVQNE 157

RESULT 7

US-10-260-576-4

Sequence 4, Application US/10260576

Publication No. US20030092130A1

GENERAL INFORMATION:

APPLICANT: YAMAMOTO, Kozo

KURIMOTO, Masashi

TITLE OF INVENTION: POLYPEPTIDES

NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADDRESS:

ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.

STREET: 419 7th Street N.W., Suite 300

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/260,576

FILING DATE: 01-Oct-2002

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/982,285

FILING DATE: <Unknown>

APPLICATION NUMBER: JP 333,037/96

FILING DATE: No. US20030092130A1ember 29, 1996

APPLICATION NUMBER: JP 20,906/97

FILING DATE: January 21, 1997

APPLICATION NUMBER: JP 10,053,503

FILING DATE: No. US20030092130A1ember 14, 1997

ATTORNEY/AGENT INFORMATION:

NAME: BROWDY, Roger L.

REGISTRATION NUMBER: 25,618

REFERENCE/DOCKET NUMBER: YAMAMOTO-15

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-628-5197

TELEFAX: 202-737-3528

Db 121 EGYFLACEKERDLFKLILKKEDELGDRSINFTVQNE 157

RESULT 6

US-10-094-153-2

Sequence 2, Application US/10094153

Publication No. US20020169291A1

GENERAL INFORMATION:

APPLICANT: Dinarello, Charles

Query Match 99.9%; Score 811; DB 13; Length 157;

Best Local Similarity 99.4%; Pred. No. 3.1e-81;

Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFILSMYKDSQPRGM 60

Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFILSMYKDSQPRGM 60

Qy 61 AVTISVKCEKISLSCENKIISEKMNPPDNKDKTSIIFFQRSVPGHNDKMQFESSY 120

Db 61 AVTISVKCEKISLSCENKIISEKMNPPDNKDKTSIIFFQRSVPGHNDKMQFESSY 120

Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSINFTVQNE 157

Db 121 EGYFLACEKERDLFKLILKKEDELGDRSINFTVQNE 157

RESULT 6

US-10-094-153-2

Sequence 2, Application US/10094153

Publication No. US20020169291A1

GENERAL INFORMATION:

APPLICANT: Dinarello, Charles

```

; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 157 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-260-576-4

Query Match          99.9%; Score 811; DB 14; Length 157;
Best Local Similarity 99.4%; Pred. No. 3.1e-81;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDNRNAPRTIFIISMYKDSQPRGM 60
DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDNRNAPRTIFIISMYKDSQPRGM 60

QY 61 AVTISVKCKISXLSCKENKIISFKEMNPPDNIKDTKSDIIFQRSVPGHDNKKMFESSY 120
DB 61 AVTISVKCKISTLSCENKIISFKEMNPPDNIKDTKSDIIFQRSVPGHDNKKMFESSY 120

QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
DB 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157

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RESULT 8
US-10-297-136-1
; Sequence 1, Application US/10297136
; Publication No. US20030113292A1
; GENERAL INFORMATION:
; APPLICANT: ESSER, KLAUS M.
; APPLICANT: ROSENBERG, MARTIN
; APPLICANT: TAL-SINGER, RUTH
; APPLICANT: WOODNUTT, GARY
; APPLICANT: CHISARI, FRANCIS V.
; APPLICANT: DILLON, SUSAN B.
; TITLE OF INVENTION: Methods of Treating Viral Diseases with
; FILE REFERENCE: P51144
; CURRENT APPLICATION NUMBER: US/10/297,136
; CURRENT FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: PCT/US01/17924
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: 60/208,869
; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-297-136-1

```

```

Query Match          99.9%; Score 811; DB 14; Length 157;
Best Local Similarity 99.4%; Pred. No. 3.1e-81;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDNRNAPRTIFIISMYKDSQPRGM 60
DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDNRNAPRTIFIISMYKDSQPRGM 60

QY 61 AVTISVKCKISXLSCKENKIISFKEMNPPDNIKDTKSDIIFQRSVPGHDNKKMFESSY 120
DB 61 AVTISVKCKISTLSCENKIISFKEMNPPDNIKDTKSDIIFQRSVPGHDNKKMFESSY 120

QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
DB 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157

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RESULT 9
US-10-312-491-3

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```

; Sequence 3, Application US/10311491
; Publication No. US20030143198A1
; GENERAL INFORMATION:
; APPLICANT: Johanson, Kyung O.
; APPLICANT: Kirkpatrick, Robert B.
; APPLICANT: Shatzman, Allan R.
; APPLICANT: Ho, Yen Sen
; APPLICANT: McDevitt, Damien
; TITLE OF INVENTION: Method for Preparing a Physiologically
; FILE REFERENCE: P51137
; CURRENT APPLICATION NUMBER: US/10/311,491
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/US01/18804
; PRIOR FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: 60/211,832
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/224,128
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/264,923
; PRIOR FILING DATE: 2001-01-20
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-311-491-3

```

```

Query Match          99.9%; Score 811; DB 14; Length 157;
Best Local Similarity 99.4%; Pred. No. 3.1e-81;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDNRNAPRTIFIISMYKDSQPRGM 60
DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDNRNAPRTIFIISMYKDSQPRGM 60

QY 61 AVTISVKCKISXLSCKENKIISFKEMNPPDNIKDTKSDIIFQRSVPGHDNKKMFESSY 120
DB 61 AVTISVKCKISTLSCENKIISFKEMNPPDNIKDTKSDIIFQRSVPGHDNKKMFESSY 120

QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
DB 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157

```

```

RESULT 10
US-10-397-786A-3
; Sequence 3, Application US/10397786A
; Publication No. US20040018195A1
; GENERAL INFORMATION:
; APPLICANT: Griswold, Donald
; APPLICANT: Li, Li
; APPLICANT: Li, Jian
; TITLE OF INVENTION: DIABETES DISEASE DERIVED PROTEINS, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN-0287
; CURRENT APPLICATION NUMBER: US/10/397,786A
; CURRENT FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: 60/367,902
; PRIOR FILING DATE: 2002-03-26
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patent In Ver 2.0
; SEQ ID NO 3
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-397-786A-3

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```

Query Match          99.9%; Score 811; DB 15; Length 157;
Best Local Similarity 99.4%; Pred. No. 3.1e-81;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDNRNAPRTIFIISMYKDSQPRGM 60

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Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTDSDCRNAPRTTIIISMYKDSQPRGM 60
Qy 61 AVTISVKCEKISXLSKCNKIISFKEMNPPDNIKDTSKDIFFORSVFGHDKMKQFESSY 120
Db 61 AVTISVKCEKISXLSKCNKIISFKEMNPPDNIKDTSKDIFFORSVFGHDKMKQFESSY 120
Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 11
US-10-280-609-1
; Sequence 1, Application US/10280609
; Publication No. US2004002336A1
; GENERAL INFORMATION:
; APPLICANT: Heavner, George
; APPLICANT: Snyder, Linda Anne
; APPLICANT: McCarthy, Stephen G.
; TITLE OF INVENTION: IL-18 OR MUT-IL-18R PROTEINS, ANTIBODIES, COMPOSITIONS,
; FILE REFERENCE: CEN0321
; CURRENT APPLICATION NUMBER: US/10/280,609
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: 60/335,880
; PRIOR FILING DATE: 2001-10-26
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent In Ver 3.1
; SEQ ID NO 1
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-280-609-1

Query Match 99.9%; Score 811; DB 16; Length 157;
Best Local Similarity 99.4%; Pred. No. 3.1e-81;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTDSDCRNAPRTTIIISMYKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTDSDCRNAPRTTIIISMYKDSQPRGM 60
Qy 61 AVTISVKCEKISXLSKCNKIISFKEMNPPDNIKDTSKDIFFORSVFGHDKMKQFESSY 120
Db 61 AVTISVKCEKISXLSKCNKIISFKEMNPPDNIKDTSKDIFFORSVFGHDKMKQFESSY 120
Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 12
US-10-646-308-14
; Sequence 14, Application US/10646308
; Publication No. US20040136992A1
; GENERAL INFORMATION:
; APPLICANT: BURTON, Paul B. J.
; APPLICANT: DELISHER, Theresa A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING CARDIOVASCULAR DISEASE
; FILE REFERENCE: 3432-B
; CURRENT APPLICATION NUMBER: US/10/646,308
; CURRENT FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: --to be assigned--
; PRIOR FILING DATE: 2003-08-12
; PRIOR APPLICATION NUMBER: 60/406,418
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 14
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapiens
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US-10-646-308-14

Query Match 99.9%; Score 811; DB 16; Length 157;
Best Local Similarity 99.4%; Pred. No. 3.1e-81;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTDSDCRNAPRTTIIISMYKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTDSDCRNAPRTTIIISMYKDSQPRGM 60
Qy 61 AVTISVKCEKISXLSKCNKIISFKEMNPPDNIKDTSKDIFFORSVFGHDKMKQFESSY 120
Db 61 AVTISVKCEKISXLSKCNKIISFKEMNPPDNIKDTSKDIFFORSVFGHDKMKQFESSY 120
Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 13
US-10-695-195-7
; Sequence 7, Application US/10695195
; Publication No. US20040068099A1
; GENERAL INFORMATION:
; APPLICANT: Timans, Jacqueline C.
; TITLE OF INVENTION: Mammalian Cytokines; Related Reagents and Methods
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESS: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/695,195
; FILING DATE: 27-Oct-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/398,412
; FILING DATE: 17-Sep-1999
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DXO904K
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650)852-9196
; TELEFAX: (650)496-1200
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 158 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-695-195-7

Query Match 99.9%; Score 811; DB 12; Length 158;
Best Local Similarity 99.4%; Pred. No. 3.1e-81;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTDSDCRNAPRTTIIISMYKDSQPRGM 60
Db 2 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTDSDCRNAPRTTIIISMYKDSQPRGM 61
Qy 61 AVTISVKCEKISXLSKCNKIISFKEMNPPDNIKDTSKDIFFORSVFGHDKMKQFESSY 120
```

Db 62 AVTISVKCEKISTLSCENKIISFKEMNPPDNIKDTKSDIIFQSVPGHDNKKQFESSY 121  
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157  
Db 122 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 158

## RESULT 14

US-10-694-978-7  
; Sequence 7, Application US/10694978  
; Publication No. US20040087766A1  
; GENERAL INFORMATION:  
; APPLICANT: Timans, Jacqueline C.  
; TITLE OF INVENTION: Mammalian Cytokines; Related Reagents and Methods  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA: US/10/694,978  
; APPLICATION NUMBER: US/10/694,978  
; FILING DATE: 27-Oct-2003  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/398,412  
; FILING DATE: 17-Sep-1999  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ching, Egin P.  
; REGISTRATION NUMBER: 34,090  
; REFERENCE/DOCKET NUMBER: DX0904K  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650)852-9196  
; TELEFAX: (650)496-1200  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 158 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:  
US-10-694-978-7

Query Match 99.9%; Score 811; DB 16; Length 158;  
Best Local Similarity 99.4%; Pred. No. 3.1e-81;  
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDNDNAPRTIFIISMYKDSQPRGM 60  
Db 2 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDNDNAPRTIFIISMYKDSQPRGM 61  
QY 61 AVTISVKCEKISXLSKENKIISFKEMNPPDNIKDTKSDIIFQSVPGHDNKKQFESSY 120  
Db 62 AVTISVKCEKISTLSCENKIISFKEMNPPDNIKDTKSDIIFQSVPGHDNKKQFESSY 121  
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157  
Db 122 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 158

## RESULT 15

US-10-247-703-69  
; Sequence 69, Application US/10247703  
; Publication No. US20030063597A1  
; GENERAL INFORMATION:

; APPLICANT: Branigan, Patrick  
; APPLICANT: Goletz, Theresa J  
; APPLICANT: Knight, David M  
; APPLICANT: McCarthy, Stephen G  
; APPLICANT: Scallion, Bernard J  
; APPLICANT: Snyder, Linda A  
; TITLE OF INVENTION: NUCLEIC ACID VACCINES USING TUMOR ANTIGEN ENCODING NUCLEIC ACIDS  
; FILE REFERENCE: CEN310  
; CURRENT APPLICATION NUMBER: US/10/247,703  
; CURRENT FILING DATE: 2002-09-20  
; PRIOR APPLICATION NUMBER: 60/328,371  
; PRIOR FILING DATE: 2001-10-10  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 69  
; LENGTH: 177  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-247-703-69

Query Match 99.9%; Score 811; DB 12; Length 177;  
Best Local Similarity 99.4%; Pred. No. 3.6e-81;  
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDNDNAPRTIFIISMYKDSQPRGM 60  
Db 21 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDNDNAPRTIFIISMYKDSQPRGM 80  
QY 61 AVTISVKCEKISXLSKENKIISFKEMNPPDNIKDTKSDIIFQSVPGHDNKKQFESSY 120  
Db 81 AVTISVKCEKISTLSCENKIISFKEMNPPDNIKDTKSDIIFQSVPGHDNKKQFESSY 140  
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157  
Db 141 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 177

Search completed: August 19, 2004, 13:38:12  
Job time : 46 secs